1, Appli 23, Appl 9, Appli 1, Appli

59, Appl 80, Appl Appli 9, App

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Post-processing: Minimum Match 0%
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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                    US-09-750-580-1

US-08-687-080-111

US-09-210-748A-3

US-09-099-913-1

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US-09-341-587-7

US-08-965-048-6

US-08-965-048-6

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US-08-965-048-6

US-08-658-136-2

US-08-658-136-1

US-08-658-136-1

US-08-975-080-35

US-09-916-6948-3

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US-09-916-6948-3

US-09-918-92-332

US-09-914-154-3

US-09-797-906-3

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US-09-914-154-3

US-09-9131-817-3

US-09-9131-817-3

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US-09-791-211-10
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39, Appli
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Patent No. 639973
Patent No. 639973
PATENT INFORMATION:
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
FILE REFERENCE: GENSET: 031A
CURRENT APPLICATION NUMBER: US/09/345,882
PRIOR PILLO BATE: 1999-06-30
PRIOR PILLO BATE: 1999-06-30
PRIOR PILLO BATE: 1998-06-30
PRIOR FILLO BATE: 1998-06-30
PRIOR PILLO BATE: 1998-12-10
PRIOR PILLO BATE: 1998-12-10
PRIOR PILLO BATE: 1998-12-10
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US-09-345-882-1/c
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SEQ ID NO 1
LENGTH: 162450
     OTHER INFORMATION: 5-130-257 :
    FEATURE:
                                  NAME/KEY: allele
                                                         LOCATION: 97152
OTHER INFORMATION:
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LOCATION: 88073
OTHER INFORMATION: 5
                        LOCATION:
                                                                          NAME/KEY: allele LOCATION: 97152
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LOCATION: 97122
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LOCATION: 93714
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LOCATION: 90842
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                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 5-124-273 : polymorphic base
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 162450
TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 72794
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6.2 14747
6.2 15977
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6.1 49136
6.1 162450
6.1 11558
6.1 1704
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6.1 187350
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US-09-370-265-8
US-09-608-285A-42
US-09-608-285A-59
US-09-608-285A-59
US-09-347-114A-80
US-09-347-114A-80
US-09-345-889-1
US-09-345-882-1
PCT-US93-06251-23
US-09-078-294-9
US-08-076-011-1
US-08-076-011-1
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US-08-375-841A-43
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Sequence 3, Appli
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OTHER INFORMATION: 5-133-375 :
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LOCATION: 106940
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OTHER INFORMATION:
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LOCATION: 99117
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LOCATION: 103806
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LOCATION: 108308
OTHER INFORMATION: 5-135-357
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LOCATION: 108471
OTHER INFORMATION:
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LOCATION: 134134
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LOCATION: 134374
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OTHER INFORMATION:
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LOCATION: 146328
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LOCATION: 146345
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                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352
                                                                                                                                                                                                                                                                                           NAME/KEY: allele
                                                                                     NAME/KEY: allele
LOCATION: 88050..88096
                                                                                                                                        NAME/KEY: allele
                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 72771.
                                                                                                                                                                                                            FEATURE:
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                        LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
                                                                      LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
                                                                                                                        OTHER INFORMATION:
NAME/KEY: allele
                                        NAME/KEY: allele
LOCATION: 88050.
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NAME/KEY: allele LOCATION: 90819...
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OTHER INFORMATION: complement polymorphic fragment 99-1437-325
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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LOCATION: 97099...
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LOCATION: 97130..97177
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LOCATION: 97130.
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OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: polymorphic fragment 5-130-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: 99075...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 103/83...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: 99094..99140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: 103783..103828
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
                                                                                                                                                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                                                                                                                                            NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                    OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 106918..106966
                                                      OTHER INFORMATION:
                                                                      NAME/KEY: allele
LOCATION: 108084.
                                                                                                                                                       NAME/KEY: allele
                                                                                                                                                                          FEATURE
                 NAME/KEY: allele
                                     FEATURE:
LOCATION: 108127..108177
                                                                                                                                      OCATION:
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                                                                                                                                        108084..108130
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                                                                                                                                                                                                                                                                                    .106966
                                                                           .108130
                                                                                                                                                                                                                                                              polymorphic fragment 5-133-375 SEQ ID37
                                                                                                                                                                                                                                                                                                                                                                                                    polymorphic fragment 5-131-395
                                                     polymorphic fragment 5-135-155 SEQ ID59
                                                                                                                       polymorphic fragment 5-135-155 SEQ ID38
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US-09-791-211-10
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OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 10
LENGTH: 98844
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                      NAME/KEY: unsure
LOCATION: 89049
                                         OTHER INFORMATION: unknown
                                                                                 NAME/KEY: unsure
LOCATION: 65471
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09791211 Fatent No. 6448080 (GENERAL INFORMATION)
                                                           NAME/KEY: unsure LOCATION: 87130
                                                                                                                           NAME/KEY: unsure
LOCATION: 65470
OTHER INFORMATION: unknown
                                                                                                                                                                       OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
                                                                                                                                                                                           NAME/KEY: unsure LOCATION: 65469
                                                                                                                                                                                                               OTHER INFORMATION: unknown
                                                                                                                                                                                                                                    NAME/KEY: unsure LOCATION: 65468
                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: 24962
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                              OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: 64383
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96095 CTATTAAAAATATAAAAATTAGCTGGGTGTGGTGGTGCATGCCTGTAGTCCCAGCTACTC 96036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2236 TCTCAT 2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2176 AAAAAACCACATAACATAAATTTATCATCTCGACCACTTTTCAGTTCAGTGGCATTCACA 2235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2056 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTTGGAGGTTGCAGTGAGCTGAGA 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1996 CTACTAAAAATATAAAAATTAGCTGGGTGGTGGTGGGTGCCTGTAATCCCCAGCTACAT 2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
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LOCATION: 108127..108177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.7%; Score 150; DB 4; Length 162450; 75.6%; Pred. No. 1.9e-21; rative 0; Mismatches 60; Indels 0;
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APPLICATION NUMBER: 08/272,351
FILING DATE: 8-JULY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/032,978
FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5856091man D.
REGISTRATION NUMBER: 30,946
                                                                                                      TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: (
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US-08-370-319C-12
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                               FEATURE:
                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: US-09-791-211-10
                                                                                                                                        REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                      FILING DATE: 10-JANUAKY 1350
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
OTHER INFORMATION: The sequence is preceded by
                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Bron-Falleur, Tatla; W lfel, Thomas; Coulie, Pierre;
APPLICANT: Boon-Falleur, Thierry; De Plaen, Etlenne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2056 GGGAGGCTGAGGCATGAGATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115
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New York City
                                                                                                                                                                                                                                                                                                                                                                                                                 10022
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                                                                                                                                   (212)
                                                                                                                                                                                                                                                                                                                                                                      IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                      Diskette, 5.25 inch, 360 kb storage
                                                                                                                              688-9200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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US-08-370-319C-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997 TACTAAAAATATAAAAATTAGCTGGGTGGTGGTGGTGGTGCCTGTAATCCCCAGCTACATG 2056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2965 TACTAAAAATACAAAAATTAGCCAAGCGTGGTGGTGCATGCCTGTAATCCCAGCTACTTG 3024
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                                                                                                                                 ETLING DATE: 18 MAR-193
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 620111man
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2117 TGCGCCACTGCACTCCAGTCTGGTCGGCAAGAGTGAGACTCCGTCTCAAAAACAAAACAA 2176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Traversari, Catia; W lfel, Thomas; Coulie, Pierre;
APPLICANT: Boon-Falleur, Thierry; De Plaen, Etienne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE TUTILE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2177 AAAAACCACATAACATAAAT 2196
                                                              TELEFAX: (212) 838-3984
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3 OTHER INFORMATION: kilobases
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-D
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/224,834
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                             APPLICATION NUMBER:
TOPOLOGY: linear
                    STRANDEDNESS:
                                                   LENGTH:
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                                nucleic acid
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805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                       4129 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PS/2
                                                                                                                           (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                            No. 6201111man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 148.8; DB 2;
84.0%; Pred. No. 1.8e-21;
ative 0; Mismatches 32;
                    double
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                                                                                                                                                               LUD 5377.1
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-09-224-834-12
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                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-21
PRIOR PPLICATION NUMBER: PCT/IB99/02058
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 1, Application US/09750580 patent No. 6455280 /
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWT FILE REFERENCE: 89.US2.CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997 TACTABABATTATABABATTAGCTGGGTGTGGTGGTGGGTGCCTGTBATCCCCAGCTBCATG 2056
                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2965 TACTAAAAATACAAAAATTAGCCAAGCGTGGTGGTGCATGCCTGTAATCCCAGCTACTTG 3024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2117 TGCGCCACTGCACTCCAGTCTGGTCGGCAAGAGTGAGACTCCGTCTCAAAAAACAAAACAA
                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3145 TAAAATAAAATTACATAAGT 3164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3085 AGTGCCACTGCAGCCTGGGGAGACAAGAGCAAAACTCCATCTCAAAAATAAA 3144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2177 AAAAACCACATAACATAAAT 2196
                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: 10946..12946
                                                                  LOCATION: 12947..12958
OTHER INFORMATION: exon 1
                                                                                                                    OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                            ORGANISM: Homo sapiens
               LOCATION: 13470..13526
OTHER INFORMATION: exon 2
                                                                                                       NAME/KEY: exon
                                                    NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n 6.6%;
Similarity 84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bihain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bour, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yen, Frances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bougueleret, Lydie
Ebbets-Reed, Dana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Denison, Blake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duclert, Aymeric
                                   13470..13526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is preceded by an unsequenced portion of from 4.7 to 5.3 kilobases
                                                                                                                                                                                                                                                                                                                             US 60/141,032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 148.8; DB pred. No. 1.8e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 4129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
                      NAME/KEY: primer_bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind LOCATION: 12348..12366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
                                                                                                                                                                                                                                      NAME/KEY: primer_bind LOCATION: 76644..76664
                                                                                                                                                                                        NAME/KEY: primer_bind
LOCATION: 77166..77185
                                                                                                                                                                                                                    OTHER INFORMATION: 20-853.pu
                                                                                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                                                                                       NAME/KEY: primer_bind
LOCATION: 45863..4588
                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KBY: primer_bind
LOCATION: 42070.42090
OTHER INFORMATION: 20-841.pu
                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  VAME/KEY: primer_bind
OCATION: 42572..42591
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 17-41.rp complement
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LOCATION: 12581..1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 17-42.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: 12029..1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: 20-828.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: primer_bind
LOCATION: 929..949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: 20-853-415 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 77058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THER INFORMATION: 20-842-115 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 20-841-149 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
OCATION: 45442
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LOCATION: 42218
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LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 15969..17969
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: exon 4
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LOCATION: 14271..15968
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                                                                                                                                                                                                                                                                20-842.rp
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                                                                                                                                                                                                                                                              complement
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Sequence 111, Application US/08687080
Patent No. 5965427K
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
                                                                                                  RESULT 6
US-08-687-080-111
                                                                                                                                                       Db 64741 AAAAAATAAATAAATA 64726
                                                                                                                                                                                                                                                      Db 64861 AGGAGGCTGAGGCAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGA 64802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-750-580-1
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 164; Conserva
                                                                                                                                                                                              APPLICANT: Gregory Dolganov TITLE OF INVENTION: Human R
                                                                                                                                                                                                                                                                                                                  64921 CTATTAAAAATACAAAATTAGCCGGGCATGGTGGCAGGAGCCTGTAATCCCAGCTACTC 64862
                                                                                                                                                                                    2176 AAAAAACCACATAACA 2191
                                                                                                                                                                                                                2116 TTGCGCCACTGCACTCCAGTCTGGTCGGCCAAGAGTGAGACTCCGTCTCAAAAACAAAACA 2175
                                                                                                                                                                                                                                                                         2056 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115
                                                                                                                                                                                                                                                                                                                                   1996 CTACTAAAAATATAAAAATTAGCTGGGTGGTGGTGGGTGCGTGTAATCCCAGCTACAT 2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_binding
LOCATION: 77046.77070
OTHER INFORMATION: 20-853-415.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_binding LOCATION: 45430. 45454 OTHER INFORMATION: 20-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_binding
LOCATION: 42206. 42230
OTHER INFORMATION: 20-841-149.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_binding LOCATION: 15229..15253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_binding LOCATION: 12335..12359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_binding LOCATION: 1227..1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 20-853-415.mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: primer_bind LOCATION: 77059..7707
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LOCATION: 77039..7705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 20-842-115.mis complement
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LOCATION: 45423..4544
OTHER INFORMATION: 20
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LOCATION: 42219.4223
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LOCATION: 42199..42217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 17-41-250 mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: primer_bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-842-115.probe
Human RAD50 Gene and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                6.4%;
83.7%;
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 Mismatches

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COUNTRY:

USA

94306 CA ADDRESSEE:

Gaps

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INDIVIDUAL ISOLATE: INTRON 23 OF RAD50 GENOMIC SEQUENCE US-08-687-080-111
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                              sequence 3, Application US/09210748A Patent No. 6335156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                    GENERAL INFORMATION:
APPLICANT: Hermeking, Heiko
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
APPLICANT: Kinzler, Kenneth
ITTLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
FILE REFERENCE: 1107.77810
CURRENT APPLICATION NUMBER: US/09/210.748A
CURRENT EILING DATE: 1998-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1996 CTACTAAAAATATAAAAATTAGCTGGGTGTGGTGGGTGGCTGTAATCCCAGCTACAT 2055
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 17-JU
                                                                                                                                                                                                                                                                                                                                                          1023 GGGAGGCTGAGGCAGGAGTTGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGA 1082
                                                                                                                                                                                                                                                                                                                                                                                          2056 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115
                                                                                                                                                                                                                               1143 AAAAAAGAACATGCCATGCATATAT 1167
                                                                                                                                                                                                                                                               2176 AAAAAACCACATAACATAAATTTAT 2200
                                                                                                                                                                                                                                                                                             2116 TTGCGCCACTGCACTCCAGTCTGGTCGGCAAGAGTGAGACTCCGTCTCAAAAAACAAAACA 2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/592,126 FILING DATE: 26-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2448 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 6.4%; Score 144.2; DB 2; Length 2448; Local Similarity 81.5%; Pred. No. 1.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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O
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PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-210-748A-3
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US-09-009-913-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09009913 Patent No. 6087485 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 7680
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001 AAAAATATAAAAAATTAGCTGGGTGTGGTGGTGGGTGCCTGTAATCCCAGCTACATGGGAG 2060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2061 CCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGATTGCG 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5796 AGT 5798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5736 TANTAATAATAGTTGCCATCCATTCTACTGTGCTTTCCATTAACTCGTGTAATCCTCACA 5795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2181 ACCACATAACATAAATTTATCATCTCGACCACTTTTCAGTTCAGTGGCATTCACATCTCA 2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: AXYS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2241 TGT 2243
                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 650-327-3231
                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 200
CTTY; Palo Alto
                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                              NAME: Sherwood, Pamela REGISTRATION NUMBER: 3
                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                               TELEFAX: 650-327-3231
                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                  TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181;
                                 LENGTH: 72928 base pairs
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h
Similarity 74.5%;
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285 Hamilton Ave, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                               Diskette
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US-09-210-748A-3

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Matches 167; Query Match

ANTI-SENSE: HYPOTHETICAL: MOLECULE TYPE:

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RESULT 10
US-09-729-995-3
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Sequence 3, Application US/09729995
Patent No. 6426206*4,
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity
Matches 169; Conserv
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Best Local Similarity 82.4%;
Matches 164; Conservative
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SEQ ID NO 10
LENGTH: 99500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09798096 Patent No. 6399378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Donna T. Ward APPLICANT: Andrew T. Watt TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION FILE REFERENCE: RTS-0207 CURRENT APPLICATION NUMBER: US/09/798,096 CURRENT FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38836 CTACTAAAAATATAAAACTTAGCCAGGCATGGTGGTGCATGCCTGTAATCCCATCTACTT 38777
                                                                                                                                                                                                                                   43498 GGAGGCTGAGGCAGAATCGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCTGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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STRANDEDNESS: dou
TOPOLOGY: linear
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Pred. No. 4.5e-20;
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Pred. No. 3e-
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TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CL000904
CURRENT APPLICATION NUMBER: US/09/729,995
CURRENT FILING DATE: 200-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASCEQ for Windows Version 4.0
SEQ ID NO 3
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Best Local Similarity
Matches 166; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09341587 Patent No. 6346606 X
                                                                                                                                                                                                                                                                         Query Match 6.3%;
Best Local Similarity 81.3%;
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an
FILE REFERENCE: 4121-108
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver.
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TYPE: DNA
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AAAAAACCACATAACATAAATTT
                                                     TTGCGCCACTGCACTCCAGTCTGGTCGGCAAGAGTGAGACTCCGTCTCAAAAACAAAACA 2175
                                                                                                                            GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115
                                                                                                                                                                                 CTACTAAAAATACAAAAATTAGCTGGGCATAGTGGTGGGCGGCTGTAATCCCCAGCTACTT 13436
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                                    TCGTGCCACTGCACTCCAGCCTGGGTGACAAGAGCGAAACTCCATCTCAAAACAAAACAA 13556
                                                                                                           GGGAAGCTGGGGCAGGAGAATCGCTTGAACCCGGGAAGCGGAGGTTGCAGTAAGCTGAGA 13496
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81.0%;
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Pred. No. 5.4e-20;
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Pred. No. 4.5e-20;
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13557 AAGAAAAAAAAGAATTTAATATT 13579

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                                                                                                            Query Match
Best Local Similarity
Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Ereimer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-965-048-5
                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08965048 Patent No. 6323244
                                                                                                                                                                                                                                                                               FILE REFERENCE: 7853-093

CURRENT APPLICATION NUMBER: US/08/965,048

CURRENT FILING DATE: 1997-11-05

NUMBER OF SEQ ID NOS: 8
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Best Local Similarity
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                                29719 CTATTAAAAATACAAAATTAGCCAGGTGTGGTGGCGGGTGTCTGTAATCCCAGCTGCTA 29660
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APPLICANT: Freimer, Nelson
APPLICANT: Freimer, Nelson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
FILE REFERENCE: 7853-093
CURRENT APPLICATION NUMBER: US/08/965,048
CURRENT FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                 LENGTH: 45989
2056 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115
                                                     29425 AAGAGAAGAAAAGAC 29411
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ORGANISM: Homo sapiens
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                                                                                                     Score 142.2; DB 4;
Pred. No. 5.8e-20;
0; Mismatches 33;
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Pred. No. 5.8e-20;
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2056 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115

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                                                         Query Match
Best Local Similarity
Matches 158; Conserv
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                                                                                                                                                                                                                                                                  TELEPHONE: (212) 527-7
TELEFAX: (212) 753-623
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
1996 CTACTAAAAATATAAAAATTAGCTGGGTGGTGGTGGTGGTGCCTGTAATCCCAGCTACAT 2055
                                                                                                                         IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
                                                                                                                                                            HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                           MOLECULE TYPE: DN
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: CURRENT APPLICATION DATA:
CURRENT APPLICATION UMBER: US/08/323,443B
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF
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                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 12-OC CLASSIFICATION: 43
                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                NAME: Ludwig, S. Peter REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dalvy Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION
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                                                          Conservative
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                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BURN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Darby & Darby PC
                                                                                                                                                                                                                                                                              (212) 527-7700
(12) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-1994
                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                               single
                                                                    6.3%;
84.9%;
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RS, TIMOTHY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYCYSTIC KIDNEY DISEASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                              25,351
                                                         ..
                                                      Score 141.2; DB 1
Pred. No. 8.6e-20;
0; Mismatches 28
                                                                                                                                                                                                                                                                                                                    0372/0A462
                                                                               DB 1;
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                                                                             Length 31571;
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                                                                                                                                                                                                                                          Query Match 6.3%; Score 141.2; DB 3; Length 53526; Best Local Similarity 84.9%; Pred. No. 9.4e-20; Matches 158; Conservative 0; Mismatches 28; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
OUR PROCESS OF TAXABLE PROCESS OF TAXABLE PATENTIAL NUMBER OF TAXABLE PATENT APPLICATION DATA:
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CITY: FRAMINGHAM
STATE: MASSACHUSETTS
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                                                                                                                                                1657 CTACTAAAAATACAAAAATTAGCTGGGGGTGGTGCCACGCGCCTGTAATCCCCAGCTACTC 1598
                                                                                                                                                                               1996 CTACTAAAAATATAAAAATTAGCTGGGTGGTGGTGGTGGTGGCCTGTAATCCCAGCTACAT 2055
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APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2176 AAAAAA 2181
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                                                                                                                                                                                                                                                                                                                                                            LENGTH: 53526 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/658,136
                                                                               AGGAGGCTGAGACAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCTGAGA 1538
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CONNORS, TIMOTHY D
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LANDES, GREGORY M
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Qy 2176 AAAAAA 2181
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Db 1477 AACAAA 1472
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Search completed: February 14, 2003, 17:03:26 Job time : 990.267 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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Perfect score:
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2245
1 cgggcgcacaqccqc
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
em_gss_mam: *
em_gss_mus: *
em_gss_other: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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154	162.6	170.8	237.4	281.4	374.6	Score		
6.9	7.2	7.6	10.6	12.5	16.7	Match	Query	d
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AL036334	BE627856	HSDML04M6	AI510675	AA866822	AA742555	ID		
AL036334 DKFZp564P	BE627856 uu49c07.y	AJ001114 Homo sapi	AI510675 vx91b07.y	AA866822 vx91b07.r	AA742555 nx30c11.s	Description		

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546 553 692 775	643 403 568 362	425 477 487 539 453	550 623 654 762 303	915 483 459 451 488	508 634 455 538 788	620 516 546 669 749 462 843 1067
10 12 17	12 10 12 17					17 17 17 17 17 17
0 AW974363 2 BG527806 7 AG038967 2 BF691393	BF212465 AW769859 BF681348 AQ706636	AQ513367 AW410409 B45325 AW500534 BF691653	AI754064 AL041749 BM999209 AQ751585 AQ490385	BM924680 AA083003 AI086603 BM989249 BM505317	A1719298 A1057560 AG128819 AQ060912 AV754765 BM992802 BG497601	AQ425335 AQ338901 AR889995 AG147516 AZ520846 AA419179 BM551923 BM751923
EST38646 60255675 Pan trog 60224744	60181323 hk54g10. 60215653 HS_5533_	HS_5073 fh06a01 -1061-A UI-HF-B 6022483	AI754064 cr19c04.x AL041749 DKFZp434P BM999209 UI-H-DIO- AQ751585 HS_5576_B AQ490385 RPCI-11-2	BM924680 AGENCOURT AA083003 zn10a05.r AI086603 oz76d08.x BM989249 UI-H-DP0- BM505317 ig93c04.x	A1/19/298 as45n04.x A1057560 oy31a03.x AGG128819 Pan trog1 AQ060912 CIT-HSP-2 AV754765 AV754765 BM992802 UI-H-DT0- BG497601 601859491	TBI-E _2215 Oc03. Oc03. n tro CI-11 4908. _5572 ENCOU

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## ALIGNMENTS

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·	JOURNAL COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AA742555/c LOCUS DEFINITION
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.  cDNA Library Preparation: M. Bento Soares, Ph.D.  cDNA Library Arrayed by: Greg Lennon, Ph.D.  DNA Sequencing by: Washington University Genome Sequencing Center  Clone distribution: NCI-CGAP clone distribution information can be  found through the I.M.A.G.E. Consortium/LLNL at:  www-bio.llnl.gov/bbrp/image/image.html  Insert Length: 701 Std Error: 0.00  Seq primer: -40ml3 fwd. ET from Amersham	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 433)  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),	MAYA2855 AA742855.1 GI:2782137 EST. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	AA742555 433 bp mRNA linear EST 22-JAN-1998 nx30c11.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1257620 3',

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SOURCE
ORGANISM
                                                                                                                                                  ACCESSION
VERSION
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AA866822
                                                            REFERENCE
                                                                                                                                     KEYWORDS
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                                    AUTHORS
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Best Local S
Matches 417
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hes 417;
                                                                                                                                                                                                                                                                                                                                                   CCTGCCCCACTTCTCTACTCTGGAAGTCCCCGGGAGCCTCTCCTTGCCTGGTGACCTACT 2000
                                                                                                                                                                                                                                                                                                                     AAAAATATAAAAATT 2015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Ci
Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 542)
Marra, M., Hillier, L., Allen, M.,
Geisel, S., Kucaba, T., Lacy, M.,
                                                                                                                                                                                 AA866822 542 bp mRNA linear EST 16 VX91b07:r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1282549 5', similar to TR:015164 015164 TRANSCRIPTION
                                                                                                    Mus musculus
                                                                                                                                                AA866822.1
                                                                                                                     house mouse
                                                                                                                                                                AA86682
                                                                                                                                                                     INTERMEDIARY FACTOR 1. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_GC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ity sequence stop: 432.
Location/Qualifiers
                                                                                                                                                GI:2962267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%;
95.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 374.6; DB 9; Length 433; Pred. No. 1.4e-52;
                                                               Sciurognathi;
                                                                             Craniata; Vertebrata;
                   Lе,М.,
               Bowles, M., Dietri
Le, M., Martin, J.,
                            Dietrich, N., Dubuque, T
                                                             Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                             Euteleostomi; Murinae; Mus
                                                                                                                                                                                                                 EST 16-MAR-1998
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Best Local
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JOURNAL
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                                                                                                                                                                                                                                                                                     778
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                                                                                                                                                                                                                                                                                                                                                  718
                                                                                                                                                                                                                                                                                                                                                                                   658 GGGATTCAGACCATGTCAGCTTCAGTCCAGAGAGCTGTGGCCATGTCCTCCGGGGACGTC 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                  80 GGAATTCAGACCATGGCAGCTTCTGTCCAGAGAGCTGTGACCGTGGCCTCTGGGGATGTT 139
               TETECCGTGTGTCGGGACGGCGGGGGGCTCATCTGCTGTGACGGCTGCCCTCGGGCCTTC
                                                                            GTTCCCGCCCTCTGGCCCTCCCCAGTGACCCCGAGCTCCACCAGAAGAATGAGGACGAG
TGTGCCGTGTGCCACGACGGAGGTGAGCTCATCTGTTGTGACGGCTGTCCGCGGGCCTTC
                                                                                                                                          AAGGGAGCCCAGGGCGCTGCCCCCGGTGGAGGTGAGGCTAGGGTGGGCCAGCAGGGCAGC 954
                                                            GTTCCTCCCTTCCATCCCTCCCCAGTGAGCCCCCAGGTTAACC---AGAACGAGGATGAG
                                                                                                                     AAGGGAGCCCAGGTCACTATACC----TAGATGAGCAGAAAGTGGGCCAGCAGTGTGGG
                                                                                                                                                                                 AGTGGCAATTTGAAGAACAAGGCCCGGAGTGGTAGCAGCCTAAAGCCAGTGGTCCGAGCC
                                                                                                                                                                                                            --- GGCAGTGGGAAGAACAAGGCCCGCAGCAGCAGTGGCCCGAAGCCTCTGGTTCGAGCC
                                                                                                                                                                                                                                           TCCAAGAAGTGCATTCAGGTTGGGGGAGAGTTTTATACACCCAACAAGTTCGAAGACCCC
                                                                                                                                                                                                                                                            TCCAAGAAGTGCATCCAGGTTGGTGGGGAGTTCTACACTCCCAGGAAGTTCGAAGACTCC
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:674349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicinep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Thymus"
/dev_stage="4 weeks"
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/clone="IMAGE:1282549"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 281.4; DB 9; Pred. No. 3.6e-37;
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11;

Gaps

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1014

319 894 259 837 199

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**FOCUS** 

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                                                                                                                                                                                                                                Matches 353;
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       224
                                                                                                                                                         104
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                                                                                                                                                                                                                                                   Local Similarity
CCGGGAGCCCGAGGGGCCGTCGAGGGGGGATCCTCATCCAGCAGGTGTTTGAGTCAGGCGGC 777
                                                                                                                                                                         GGGATTCAGACCATGTCAGCTTCAGTCCAGAGAGAGCTGTGGCCCATGTCCTCCGGGGACGTC 717
                                     TCCAAGAAGTGCATCCAGGTTGGTGGGGAGTTCTACACTCCCAGCAAGTTCGAAGACTCC 837
                                                                          CCAGGAACCCGAGGGGCCGTGGAAGGGATCCTTATCCAGCAGGTGTTTGAGTCAGGAAGA
                                                                                                                                                   GGAATTCAGACCATGGCAGCTTCTGTCCAGAGAGCTGTGACCGTGGCCTCTGGGGATGTT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:674349
This read i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
1 (bases 1 to 588)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI510675
588 bp mRNA linear ES'vx91b07.y1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1282549 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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AI510675.1 GI:4409580
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 398
                                                                                                                                                                                                                                                                                                                      3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

a 165 c 165 g 130 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1282549"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
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                                                                                                                                                                                                                                                 10.6%;
71.9%;
                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                             Score 237.4; DB 9
Pred. No. 6.7e-30;
                                                                                                                                                                                                                              Mismatches 128;
                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                            Indels 10;
                                                                                                                                                                                                                                                               Length 588
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JOURNAL
                                                                                                                                                            Query Match
Best Local
                                                                                                                                              Matches 175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                      833
                                                                    400
   61
                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCACCTGGCCTGCCTGCCCTCCGGCTCCGGGAGATCCCCAGTGGGACCTGGAGGTGCTC 1133
                                    ACTCCGGCAGTGGGAAGAACAAGGCCCGCAGCAGCAGTGGCCCGAAGCCTCTGGTTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --TCCTCCCCTTCCATCCCTTCCCAGTGAGCCCCAGGTTAACCAGAACGAGGGATGAGTG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGGGAGCCCAGGTCACTATACCTAGATGAGCAGAAAGTGGGCCCAGCAGTGTGGGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GGCAGTGGGAAGAACAAGGCCCGCAGCAGCAGTGGCCCGAAGCCTCTGGTTCGAGCC 894
ACTCCGGCAGTGGGAAGAACAAGGNCCGNAGNAGNAGTGGCCCGAAGCCTCTGGTTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTTGCTTC 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCGTGTGCCACGACCGGAGGTGAGCCTTATCTGTTGTGACGGCTGTNCCCCGGCCCTT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGCCGTGTCTCGGGACGGCGGGGAGCTCATCTGCTGACGGCCTG-CCCTCGGGCCTT 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCCCGCCCCTCTGGCCCTCCCCAGTGACCCCCAGCTCCACCAGAAGAATGAGGACGAG 1014
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2 (bases 1 to 200)

Nagamine,K., Peterson,P., Scott,H.S., Kudoh,J., Minoshima,S.,
Heino,M., Krohn,K.J., Lalioti,M.D., Mullis,P.E., Antonarakis,S.E.,
Kawasaki,K., Asakawa,S., Ito,F. and Shimizu,N.
Mutations in a novel zinc finger protein AIR are responsible for
                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-AUG-1997) Scott H.S., Department of Genetics and Microbiology, University of Geneva Medical School, 1 rue Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
AJ001114
AJ001114.1 GI:3426119
                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune polyglandular disease type I (APECED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scott, H.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                            Conservative
                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="422.3"
                                                                                                                                                                                                                                                /note="trapped_exon"
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                            7.68;
90.78;
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                                                                                                                                                           Score 170.8; DE Pred. No. 1e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
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                        CTGCCACTTCCCAGCCGGCACCTCCCGGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTC 1547
TGCAGACTCGACTCCCACGCCAGGCACACCGGGCGAAGCTGTACCCACCTCTGGGCCCCG
                                                   CTGCCACTTCCCGACGGCCGCCGCCCGGGGGGACCAATCTCCGCTGCAAATCCTGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE627856
451 bp mRNA linear EST 24-AUG-2000 uu49c07.y1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:3375276 5' similar to TR:Q9Z0E3 Q9Z0E3 AIRE PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -40RP from Gibco
High quality sequence stop: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                              provided by Dr. Bertrand Jordan. rounds of normalization, and was Soares and M.Fatima Bonaldo."

161 c 129 g 83 t
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3375276"
/clone="1ib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                          7.2%;
71.8%;
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                                                                                                                                                                        Score 162.6; DB 10;
Pred. No. 1.8e-17;
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                 2117 TGCGCCACTGCACTCCAGTCTGGTCGGCAAGAGTGAGACTCCGGTCTGAAAAACAAAAAAA 2176
                                                                                                          2057
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            104
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                                                                                    GGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGAT 2116
                                                                                                                                  GGAGGCTGAGGCAGGAGAATCGCTTGCACCCACGAGGCGGAGGCTGCAGTGAGCTGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCCAGAGCATGTCACGCCCGCTGGCCGAGACACCACCCT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGGGACGACCTGGAGTCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGCAGTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGGCCCCTGGGCCAA------GGATGACACTGCCAGTCACGAGCCCGCTCTGCA 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by Clagen (Hilden/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone (DKFZp564PO32) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST (Duesterhoeft, et al.)
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sl sequence also available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Duesterhoeft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKFZp564P032_r1 564 (synonym: DKFZp564P032 5', mRNA sequence
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                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Charlottenburg, GERMANY; Email: clone@rzpd.de Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      /clone="DKFZp564P032"
/clone_lib="564 (synonym:'hfbr2)"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                       /note="Vector: pAMP1;
125 c 126 g
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                         /lab_host="X1-2blue"
                                                                                                                                                                                                                                                                                                                                       /dev_stage="fetal"
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81.7%;
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Pred. No. 4.2e-16;
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226 t 4 others
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                                                                                                                                                                                                  2116
                                                                                                                                                                                                                                          2056 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115
                                                                                                                                                                                                                                                                                                         1996 CTACTAAAAATATAAAAATTAGCTGGGTGGTGGTGGTGGTGCCTGTAATCCCAGCTACAT 2055
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                                                                                                   AATTAATGAATTTGCCTATATTAGGGTTCTCCA 304
                                                                                                                               AAAAAACCACATAACATAAATTTATCATCTCGA 2208
                                                                                                                                                                               TTGCGCCACTGCACTCCAGTCTGGTCGGCCAAGAGTGAGACTCCGTTCTCAAAAACAAAACA 2175
                                                                                                                                                           AAAAACCACATAAAATTTATCATCTCGACCACTT 2214
                                                                                                                                                                                                                           GGGAGGCTGAGGCACGAGAATTGCTTGAATCTGGGAGGTGGAGGTTGCAGTGAGCTGAAA
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 AQ338901 516 bp D1
HS_2215_B2_B08_MR CIT Approved Human
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Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are available from Research Genetics (info@resgen.com). BAC
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1 (bases 1 to 620)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ425335 620 bp DNA linear GSS CITBI-E1-2572112.TR CITBI-E1 Homo sapiens genomic clone
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AQ425335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hbe@tigr.org
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                        149
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of BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBeloBAC11; Site_1: CalTech Human BAC Library D" a 178 c 117 g 176 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2572112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="sperm"
/note="Vector: pBel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        6.9%;
82.6%;
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                                                                                                                                                                                                                                                                                                                                                                      Score 153.8; DB 1
Pred. No. 4.6e-16;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                     DNA
                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 620;
      Genomic
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ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2054 ATGGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTTGGAGGTTGCAGTGAGCTGA 2113
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   EST
                                                                                                                                 wm80c03.x1
similar to
                                    AI889995.1
                                                                    AI889995
                                                                                                 repetitive
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Clones may be purchased from Research Genetics (in
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2215 row: D column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 515)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Smith,K., Shartzell,S., Adams,M.D. and Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. and M.D. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 516.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 Queen Anne Avenue North, Seattle, WA 98109, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens genomic clone Plate=2215 Col=16 Row=D,
AQ338901
AQ338901.1 GI:4144917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
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/db_xref="taxon:9606"
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                                                                                                                      NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2442244 3 contains Alu repetitive element;contains element THR
                                                                                             element ;, mRNA sequence.
                                GI:5595159
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82.5%;
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Homo sapiens

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RESULT 10
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AUTHORS
TITLE
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Best Local S
Matches 169
                       AUTHORS
                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                         CAAAGAACAAAAACAAAAA 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169;
                                                                                                                                sequence.
AG147516
AG147516.1
GSS.
                   Fujiyama,A.,
   Totoki,Y., Watanabe,H.
                                                                 Eukaryota;
                                                                                  Pan troglodytes
                                                                                       Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-009H02.TJ.
                                                                                                                                                                                           Pan troglodytes DNA, clone:
                                                   Mammalia; Eutheria;
                                                                                                                                                                                                             AG147516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 748 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 546)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 427.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:2442244"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11539-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                Metazoa; Chordata;
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                                                                                                                                               GI:16677194
                  Hattori, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%;
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                                              Primates;
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Pred. No. 1.1e-15;
   and
Toyoda,A.,
nd Sakaki,Y
                                                                                                                                                                                                       669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                      RP43-009H02.TJ,
                                          Craniata; Vertebrata; Catarrhini; Hominidae;
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              Taylor, T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
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                                            Hominidae;
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                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                        genomic survey
              Yada,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ph.D.,
                                                           Euteleostomi;
                                                                                                                                                                                                     GSS 08-JAN-2002
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGGAGGTTGCGGTGAGCCGAGATGGCACCACCTGCACTCCAGCCTGGGTGACAAGAGTGA
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                  BAC end sequences of library RPCI-11 Unpublished (1997) Other_GSSs: RPCI-11-238G4.TVC
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 749)
                                                                                                                                                                                                                                   GSS.
                                                                                                                                                                                                                                                                                                   AZ520846
RPCI-11-238G4.TJ RPCI-11
                                                                                                                       Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                AZ520846.1 GI:10833356
                                                                                                                                                                                                                                                                                    DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujiyama, A., Hattori, M., To
Totoki, Y., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC end sequences of Library RPCI-43
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.Site 1. : EcoRI
R.Site 2 : EcoRI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
/ 168 c 123 g 204 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP43-009H02.TJ"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/db_xref="taxon:9598"
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79.68;
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                                                                                                                                                                                                                                                                                                   Homo
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genomic clone
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                                                                                                                     Jong, P.
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RPCI-11-238G4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 AAATACAAAAAATTAGCTGGGCGTGGTGGTGAATGCCTGTAACCCCAGCTACTTGGGAG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGAGGCAGGAGATCGCTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCCGAGATCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATAAATAAATAAATAAATGGTTGTCTCCAATAACTGCCTCCTTGGC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180;
                                                        Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                      zv34g08.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:755582 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library availability, please contact Pieter de Jong pieterdedejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tlgr.org/tdb/humgen/bac_end_search/bac_end_search.html. This BAC end was generated during the RAD process and may have higher chance of clone tracking errors.
           Washington University School of Medicine
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                              (bases 1 to 462)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBACe3.6; Site_1:
RPCIll Human Male BAC Library"
150 c 203 g 198 t
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/clone="RPCI-11-238G4"
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78.9%;
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Pred. No. 1.2e-15;
); Mismatches 48
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             St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAGGCTGAGGCAGGAGAACTGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAACCCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTACTAAAAATACAAAAATTAGCTGGGCACGGTGGTGGATGCCTGTAATCCCAGCTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGCGCCACTGCACTCCAGTCTGGTCGGCAAGAGTGAGACTCCGTCTCAAAAAACAAAACA 2175
                                                                                                                                                                                                                                                                                                          AQ741619
843 bp DNA linear GSS 16-JUL HS_5572_B2_C07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1148 Col=14 Row=F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham
                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 843)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 314 286 1810
Email: est@watson
                                                                                                            Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                      99380589
                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "
a 96 c 84 g 162 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1
strand cDNA was primed with a Not I - Oligo(dT) prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:755582"
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75.2%;
66,
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Pred. No. 1.6e-15;
JC,
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                                                                                                                Holzman,T.,
Adams,M.D. and
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KEYWORDS
SOURCE
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BM551923/c
                                                                                                COMMENT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2054 ATGGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGA 2113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAAAAGTACTAAAAGGANAGTTTATAGCTATAAAAAAAATGCCCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTACTAAAAATACAAAAATTAGCTGAGCATATTGGCGGGTGCCTGTAATCCCCAGCTAC 417
                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180;
                                                                                                             Unpublished (1999)
                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutharia; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                   DMD31343 1067 bp mRNA linear EAGENCOURT_6544650 NIH_MGC_72 Homo sapiens cDNA clone 5', mRNA Sequence
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                        BM551923.1 GI:18789359
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              cDNA Library
                                   CDNA
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: |Wallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer:
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                                                                                                                                                                                                                                                                                                                               mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
Library Preparation: Life Technologies, Inc.
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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a 164 c 145 g 345 t 3 others
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/clone_lib="RPCI-11 Human Male BAC Library"
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/db_xref="taxon:9606"
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No. 1.4e-15;
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                                                                                                                     Gene Collection (MGC)
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e IMAGE:5548252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1996 CTACTAAAAATATAAAAATTAGCTGGGTGGTGGTGGTGGTGCCTGTAATCCCAGCTACAT 2055
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                                                                                                                                                 Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: 1131007_y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
                                                                                          Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
Library was constructed by Dr. Hiroshi Inoue DNA sequencing
                    Email: dmelton@biohp.harvard.edu
                                                                Tel: 617-495-1812
                                                                                                                                                                                                                                                                    Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Carden
                                                Fax: 617-495-8557
                                                                                      MA 02138
                                                                                                                                                                                                                                                                                                                               Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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il31d07.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6031548
                                                                                                                                                                                                                                          ,M., Gibbons,M., McCann,R., Cole,R.,
, Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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301 c 227 g 266 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: skin; Vector: pCMV-SPORT6; Site_1: Site_2: Sall; Cloned unidirectionally. Primer: Average insert size 2 kb. Library constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:5548252"
/clone_1ib="NIH_MGC_72"
/clone_Lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Pred. No. 1.5e-15;
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Tsagareishvili,R., Williams,T
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Seq primer: -40Up from Gibco
High quality sequence stop: 450.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
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/lab_host="DH10B"
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## ALIGNMENTS

TITLE	REFERENCE AUTHORS	DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 A97284 LOCUS
NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING IN MUTATED FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS ECTODERMAL DYSTROPHY (APECED)	unclassiried.  1 (bases 1 to 2245) Yaspo,M. and Lehrach,H.	Sequence 1 from Patent WO9918197. A97284 A97284.1 GI:6780668 unidentified. unidentified	:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An autoimmune disease, APECED, caused by mutations in a novel gene featuring two PHD-type zinc finger domains
Nat. Genet. 17, 399-403 (1997)
2 (bases 1 to 2245)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Sapiens mRNA for AIRE prote
90
/translation="MATDAALRRLLRLHRTEIAVAVDSAFPLLHALADHDVVPEDKFQ
ETLHLKEKEGCPQAFHALLSWLLTQDSTAILDFWRVLFKDYNLERYGRLQPILDSFPK
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                                                                                                                                             /clone_
121. .
                                                                                                                                                                                                                                                             /clone="B1-1"
/tissue_type="thymus"
/clone_lib-rlambda GT11 from Clontech (cat# h15010B)"
1811. .2180
                                                      /protein_id="CAB10790.1"
/db_xref="GI:2665371"
/db_xref="SWISS-PROT:043918"
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/clone_lib="lambda GT
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                                                                                                                                                                                                                                                                                                                                /chromosome="21"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
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AGTGGGAAGAACAAGGCCCGCAGCAGCAGTGGCCCGAAGCCTCTGGTTCGAGCCAAGGGA 900
                                                                                                                                      GGAGCCCGAGGGGCCGTGGAGGGGATCCTCATCCAGCAGGTGTTTGAGTCAGCGGGCTCC
                                                                                                                      GGAGCCCGAGGGGCCGTGGAGGGGGATCCTCATCCAGCAGGTGTTTGAGTCAGGCGGCTCC
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WRCSSCLQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTL
VYKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCA
AAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAPVEGVLAPSPARLAPGPAKDDTASHE
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765 c 697 g 364 t
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GSKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQ
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841

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AGCGAGCACACCTTCGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCCCGTCCGGCG
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2 (bases
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                                                                                                                                                       /gene="APECED"
128. 1765
/gene="APECED"
/note="autoimmune 1
/TEANS 18 tion="MATDAALRRLLRLHRTEIAVAVDSAFFLLHALADHDVVPEDKFQ ETLHKEKEGCPQAFHALLSWILT90ST9A ILDEWRVLFKOY WLERYGRLOPILDSEPK DVDLSOPRKERGCROPAFHALLSWILT90SST9A ILDEWRVLFKOY WLERYGRLOPILDSEPK DVDLSOPRKERGKEPAVPKALVPPBRIPTKKKASEEARAAAPAALTPRGTASPGSQLKA KPPKKPESSAEQQRLPLGNGIQTMSASYQRAVAMSSGDVPGARGAVEGILTQQVFESG GSKKCIQVGGEFYTPEKFEDSGSGKNKARSSSGEPKPLVRAKGAQGAAPGGBERLGQQ GSVFAFHACLSPPLREIPSGTWRCSGCLQATVQEVQDFACEARGACEFVEPGLTGCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQDFACEARGACEFVEPGLTGCDGCPAFHACLSPPLREIPSGTWRCSSCLQATVQEVQDFACEARGACEFVETPLPGCLRSAGEEVRGCPGEPLAMDTTL VXKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCA
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/db_xref="GI:2696615"
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/dev_stage="3-yr-old"
1. .2027
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/dh xraf-".
                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                           /chromosome="21"
/map="21q22.3"
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Direct Submission
Submitted (16-AUG-1997) Nobuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160, Japan (E-mail:shimizu@dmb.med.keio.ac.jp, Tel:03-3351-3370, Fax:03-3351-2370)
                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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	AAGAAGTGCATCCAGGTTGGTGGGGAGTTCTACACTCCCAGCAAGTTCGAAGACTCCGGC 840	781 788	gg Qy
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0;	atch 89.9%; Score 2018.4; DB 9; Length 2027; cal Similarity 100.0%; Pred. No. 0; 2019; Conservative 0; Mismatches 1; Indels 0; Gaps	Query Ma Best Loc Matches	
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RESULT 4 AB006683 LOCUS

ACCESSION . KEYWORDS VERSION

AB006683 AB006683.1

GI:2696616

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Direct Submission
Submitted (16-AUG-1997) Nobuyoshi Shimizu, Kejo University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160, Japan (E-mail:shimizuedmb.med.keio.ac.jp, Tel:03-3351-2370, Fax:03-3351-2370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagamine, K., Peterson, P., Scott, H.S., Kudoh, J., Minoshima, S. Heino, M., Krohn, K.J.E., Lalioti, M.D., Mullis, P.E., Antonarakis, S.E., Kawasaki, K., Asakawa, S., Ito, F. and Shimiz Positional cloning of the APECED gene Nat. Genet. 17 (4), 393-398 (1997)
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a 485 c 508
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1. .1545
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/isolate="Caucasian"
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Pred. No. 2.9e-171;
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Vertebrata;
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CDS gene

/gene-" 237. .1

APECED"

/sex="male" /map="21q22.3"

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Shimizu, N.

(bases 1 to 1545)

JOURNAL

source

JOURNAL MEDLINE

98061086

TITLE

REFERENCE AUTHORS

Mammalia; Eutheria; Eukaryota;

Metazoa;

sapiens

SOURCE ORGANISM

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polyA\_signal

Matches Query Match Best Local (

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Conservative

Local Similarity

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GGACTACAACCTGGAGCGCTATGGCCGGCTGCAGCCCATCCTGGACAGCTTCCCCAAAGA 428
                                                                                                                                                                      CAGCGCCTTCCCACTGCTGCACGCCGCTGGCCTGACCACGTGGTCCCCCGAGGACAAGTT
                                                 GTCCTGGCTCCTGACCCGGGACAGTGGGGCCATCCTGGATTTCTGGAGGATTCTCTTTAA
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Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G., Huang,Y.Q.,
Detter,J.C., Davoodi-Sermiromi,A. and She,J.X.
Complete genomic sequence, gene structure and localization
mouse Aire gene
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Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G., Huang,Y.Q., Detter,J.C. and She,J.X.
Chromosomal localization and complete genomic sequence of the
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Ruan, O.G., Wang C.Y., Shi, J.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           murine autoimmune regulator gene
Autoimmunity 31 (1), 47-53 (1999)
20059142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archer
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KDVDLNOSRRGKBLAGPKAAVLPERPTKKKALEEPRATPATLASKSVSSPGSHLK
TKPPKKPDGLESOHLPGINGIQTWAASVORAAVTVASGDVPGTRGAVEGILIOQVFES
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GLWRCSCCLOGGRVQONLSQDFWSRPPELPAETPILVGLRSASEKTRGPSRELKASSDA
AVTYVNLLAPHPAAPLLEPSALCPLLSGNEGRPGPAPSARCSVCGGTEVLRCAHCA
AAFHWRCHFPTAAARPGTNLRCKSCSADSTPTPGTPGEAVPTSGPRPAPGLAKVGDDS
ASHDPVLHRDDLESLLNEHSFDGILOWAIQSMSRPLAETPPFSS"

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/db_xref="GI:7108573"
/translation="MAGGDGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism=™Mus
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CACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTCAGGAGACGTG-----AC 1559
                                            GGTGTTGCGGTGTGCACACTGTGCCGCTGCCTTCCACTGGCGCTGCCACTTCCCGACGGC 1385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1656)
Shi.J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G., Huang,Y.Q.,
Detter,J.C., Davoodi-Sermiromi,A. and She,J.X.
Complete genomic sequence, gene structure and localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1656)
Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G.,
Detter,J.C. and She,J.X.
Chromosomal localization and complete genomic murine autoimmune regulator gene (Aire)
Autoimmunity 31 (1), 47-53 (1999)
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AF128773.
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Ruan, Q.G., Wang C.Y.,
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/product="MAGGDGMLRRLLRHLTTEIAVAIDSRAFPLLERYSRLHSILDGFF
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QQCGVPPLPSLPSEPQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS
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/chromosome="10"
                                                                                                                                                          /codon_start=1
                                                                                                                                                                     /function="transcription
                                                                                                                                                                                                                      /gene="Aire"
                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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Pred. No. 1.7e-160;
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JOURNAL MEDLINE PUBMED REFERENCE

VERSION KEYWORDS SOURCE ORGANISM

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TITLE AUTHORS RESULT 6 AF128773

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                                                        ECTODERMAL DYSTROPHY (APECED)
Patent: WO 9918197-A 10 15-APR-1999;
MAX PLANCK GESELLSCHAFT (DE); YASPO
Location/Qualifiers
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NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING

NUTATED FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS
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Pred. No. 1.7e-16
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                                     Karin,B.
Direct Submission
Submitted (14-JAN-1999) Karin B.
Molecular Genetics, Thestrasse
                                                                                                                                                                l (bases 1 to 1039)
Blechschmidt,K., Schweiger,M., Wertz,K., Poulson,R.,
Christensen,H.M., Rosenthal,A., Lehrach,H. and Yaspo.
                                                                                                                                       The mouse Aire gene: comparative organization, and expression Genome Res. 9 (2), 158-166 (1999)
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 1659)
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AJ132243
AJ1322431 GI:4456674
Aire gene; Aire protein.
/organism="Mus musculus"
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3, Berlin D-14195, Ger
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 AGGGCCCGTGGAGGGGATCCTCATCCAGCAGGTGTTTGAGTCAGGCGGCTCCAAGAAGTG
                                                          CATGGCAGCTTCTGTCCAGAGAGCTGTGACCGTGGCCTCTGGGGATGTTCCAGGAACCCG
                                                                           CATGTCAGCTTCAGTCCAGAGAGCCTGTGGCCATGTCCCTCCGGGGACGTCCCGGGAGCCCG
                                                                                                                                  CAAGAAGCCGGAGAGCAGCGCAGAGCAGCAGCAGCCTTCCACTCGGGAACGGGATTCAGAC
                                                                                                                     TAAGAAGCCAGATGGCAACTTGGAGTCACAGCACCTTCCTCTTGGAAACGGAATTCAGAC
                                                                                                                                                                                           AGCAGCCCTGACTCCAAGGGGCACCGCCAGCCCAGGCTCTCAACTGAAGGCCCAAGCCCCC
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QETTLRKEKEGCPQAFHALLSWILTRDSGAILDEWRILFKDYNLERYSRLHSILDGFP
KDVDLNQSKKGRKPLAGPKAAVLPREPTKKKALEEPRATPATLASKSVSSPGSHLK
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QOCGVPPLPSLPSEPQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS
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AVTYVNLLAPHPAAPLLEPSALCPLLSAGNEGRPGPAPSARCYCGDGTEVLRCAHCA
AAFHWRCHFPTAAARPGTNLRCKSCSADSTPTPGTPGEAVPTSGPRPAPGLAKVGDDS
ASHDPVLHRDDLESLLHEHSPGILQWAIQSWSRPLAETPPFSS"
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/product="Aire protein"
/protein_id="CAB36909.1"
/db_xref="GI:4456675"
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/chromosome="10"
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REFERENCE AUTHORS TITLE

JOURNAL

JOURNAL MEDLINE PUBMED

99148139

10022980

(bases 1 to 1659)

FEATURES

source

Location/Qualifiers
1. .1659

VERSION KEYWORDS

SOURCE

Mus musculus.

gene; Aire protein.

REFERENCE

TITLE AUTHORS RESULT 8 MMU132243 LOCUS

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ACCGCCACCCAGACTCCCCACCAAGAGGAAGGCCTCAGAAGAGGCTCGAGCTGCCGCGCC
                                                           TGTGGACCTAAACCAGTCCCGGAAAGGGAGAAAGCCCCCTTGCTGGTCCCAAGGCCGCGGT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Aire gene; APECED protein.
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KEVDLNQSRKGRKPLAGPKAAVLPPRPPTKRKALEEPRATPPATLASKSVSSPGSHLK
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GRSKKCIQVGGEFTTPHKFEDDPSGULKNKRAGGSSLKPPVRAKGAQVTIGRBDZKVG
QCGVPPLPSLPSEPQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS
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AVTYVNILAPHPAAPLLEPSALCPLLSAGNEGREGPAPSARCSVCGDGTEVLRCAHCA
AAFHWRCHFPTAAARPGTNLRCKSCSADSTPTPGTPGEAVPTSGPRPAPGLAKVGDDS
ASHDPVLHRDDLESLLMEHSFDGILQWAIQSMSRPLAETPPFSS*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-JUL-1998) Pathology, Immunology and Laboratory Medicine, University of Florida, 1600 SW Archer Road, Gainesville, FL 32610, USA
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Wang,C.Y., Shi,J.D., Davoodi-Semiromi,A. and She,J.X.
Cloning of Aire, the mouse homologue of the autoimmune regulator (AIRE) gene responsible for autoimmune polyglandular syndrome type 1 (ASP1)
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Wang,C.Y., Shi,J.D., Davoodi-Semiromi,A. and She,J.X.
Direct Submission
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        Conservative
                                                                                                /Product="autoimmune regulator"
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/product="autoimmune regulator"
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GRSKKCIQVGGEFYFPMKFEDPSGNLKMKARSGSSLKPVFRAKGAQVTIPGRDEOKVG
QOCGVPPLPSILPSEPQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS
GLWRCSCCLQGRVQQNLSQPEYSRPPELPAETPILVGLRSASEKTRGBSRELKAXSDA
AVTYNNLLAPHPAAPLLEPSALCPLLSAGNEGRPGPAPSARCSVCGDGTEVLRCAHCA
AAFHWRCHFPTAAARPGTNLRCKSCSADSTPTGTPGETPGEAVPTSGPRAAGLKVGDDS
ASHDDYLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPPESS"

08 a 609 c 568 g 351 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Aire"
58. .1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="thymus"
1. .1936
                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/strain="B6"
                                                                                                                                                                                                                                                                                                                                                                                                            function="transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Aire"
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                       42.9%;
76.0%;
      0;
Score 964.2; DB 10;
Pred. No. 1.6e-160;
0; Mismatches 373;
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1445	GCCGCCGGGGGACCAATCTCCGCTGCAAATCCTGCTCTGCAGACTCG	1386	DЬ
	CCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTCAGGAGACGTG	50	γQ
1505 1385	CGTGCTGCGGTGTACTCACTGCGCCCCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGG	1446 1326	P O
1445 1325	GAGGGGCGCCAGGTCCAGCACCAAGCGCGCGATGCAGTTGTGGGAGATGGTACGA	26	da G
.26	GLAGGTCACACACACATACATACATACACACACACACACACA	1212	8
8	GCAGCCCCCCTGCCAGGGCTGGACTCCTCGGCCCTGCACCCCCTACTGTGTGTG	1326	Q
1325 1211	GCTCAAAGCCAGCTCTGATGCTGCTGTCACATAT	15	B 7
.15	AGAGACCCCGATCCTCGTGGGACTGAGGTCAGCTTCAGAGAAAAACCAGGGGCCCATCC	96	S B
1265	GAGACCCCGCTCCCCCCGGGGCTTAGGTCGGCGGAGAGGAGGTAAGAGGTCCACC	1206	Qy VQ
9	GGGCAGAGTCCAACAGAACCTGTCCCAGCCTGAGCTGTCCAGGCCCCCGGAGCTACCTG	03	ф
ن د	GGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCCGGCCCCCAAGGAGCCC	1146	γQ
1031	CTGTGCCCACCTCTGCAGGAGATCCCCAGTGGCCTCTGGAGATGCTCCTGCTGCAGGAGATCCCCAGTGGCCTCTGAGATGCTCCTGCAGAGAGATCCCCAGTGGCCTTGAGAGATGCTCTGAGAGATGCTCTGAGAGAGA	7	당.
<u>.</u>	CCTGTCCCCTCGCCTCCGGGAGATCCCCAGTTGGGACCTGGGGGGGG	1086	οy
<b>⊢</b>	CCAC	912	р
_	TCGGGACGGCGGGAGCTCATCTGCTGTGACGCCTGCCCTCGGGCCTTCCACCTGGCC	1026	Qγ
1025 911	TCTGGCCCTCCCCAGTGACCCCCAGCTCCACCAGAAGAATGAGGACGAGTGTGCCGTGTG	966 852	β δ
851	GGTCACTATACCTGGTAGAGAT(	9	DЬ
965	GGGCGCTGCCCCGGTGGAGGTGAGGCTAGGCTGGGCCAGCAGGGCAGCGTTCCCGCC	906	Qy
9	TGGT	73:	В
905	GAAGAACAAGGCCCGCAGCAGCAGTGGCCCGAAGCCTCTGGTTCGAGCCAAGGGAGCCC	846	Qy
731	CATTCAGGTTGGGGGAGI		ф
	ATCCAGGTTGGTGGGGGGGGTGTGGGGGGGGGGGGGGGG	œ	Ŷ
788	New York   New York	61:	B 3
نتز	CATGGCAGCTTCTGTCCAGAGAGCTGTGACCGTGGCCTCTGGGGATGTTCCAGGAACCC	ວ ດ	B B
728	TCAGCTTCAGTCCAGAGAGCTGTG	6	Q
	ATGGCAACTTGG	49	Д
668	GAAGCCGGAGAGCAGCGCAGAGCAGCAGCGCCTTCCACTCGGGAACGGGATTCAGA	60	Qy
9		43	망
5 (	GCAGCCCTGACTCCAAGGGGCACCGCCAGCCCAGGCTCTCAACTGAAGGCCAAGCCCC	54	γQ
431		37	망

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129 GGACGCGGCGTACGCCGGCTTCTGAGGCTGCACCGCACGGAGATCGCGGTGGCCGTGGA 188

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GGAGACCCCGCTCCCCCCGGGCTTAGGTCGGCGGGAGAGGAGGTAAGAGGTCCACCTGG
                                                 GGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAAGGAGCCCCCGGGCCCCAGGAGCCACCCGT 1205
                                   GGGCAGAGTCCAACAGAACCTGTCCCAGCCTGAGGTGTCCAGGCCCCCGGGAGCTACCTGC 1148
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                                                                                                                                                                                                                                                                                                        Submitted (12-FEB-1999) Pathology, (Archer Road, Gainesville, FL 32610, Location/Qualifiers
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AF128115
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an,Q.G., Wang,C.Y.,
                                                       /gene-"Aire"
58. .1713
                                                                                                                                       /db_xref="taxon:10090"
/chromosome="10"
/map="between D10Mit31
/gene="Aire"
/function="transcription
                                                                                                                                                                                                                            /strain="B6"
                                                                                                                                                                                                                                                      organism="Mus musculus"
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                 GAAGAACAAGGCCCGCAGCAGCAGTGGCCCGAAGCCTCTGGTTCGAGCCAAGGGAGCCCA
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QETLRUKEKECCPQAFHALLSWLLTRDSGAILDEWRILTRXYNLERYSRLHSILDGEF
KDVDLNQSRGKGRKELAGPKAAVLPPARPTKKALEEPRATPPATLASKSVSSPGSHLK
TKPPKKPDGNLESQHLPLGNGIOTMAASVQRAVTVASGDVVGTGGAVGILLQQVFES
GRSKKCIQVGGEFYPNKFEDDSGNLKNKARSGSSLKPVVRAKGAQVTIPGRDEQKVG
QOGGVPPLBSLPSEPQVNQNEDECAVCHDGGELICCDGCPRAFHLLACLSPLQEIPSG
LWRCSCLQGRVQQNLSQPEVSRPPELCAETPILVGLRSASEKTRGPSFELKASSDA
ATYVUNLAPHPAAPLLEPSALCPLSAANEGRPGPAPSARCSVCGDGTEVLRCAHCAA
AFHWRCHFFTAAARPGTNLRCKSCSADSTPTPGTPGEAVPTSGPREAPGLAKVGDDSA
AFHWRCHFFTAAARPGTNLRCKSCSADSTPTPGTPGEAVPTSGPREAPGLAKVGDDSA
SHDPVLHRDDLESLLMEHSFOGILQWAIQSMSRPLAETPPFSS"

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                                               Mus musculus autoimmune regulator (Aire) spliced product 1c, complete cds. AF128116
AF128116.1 GI:7108533
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                              ACCGCCACCCAGACCCACCAAGAGGGAAGGCCTCAGAAGAGGCTCGAGCTGCCGCGCC
                                                                  TGTGGACCTAAACCAGTCCCGGAAAAGGGAGAAAGCCCCCTTGCTGGTCCCAAGGCCGCGGT
                                                                                    TGTGGACCTCAGCCAGCCCCGGAAGGGGAAGCCCCCCGGCCGTCCCCAAGGCTTTGGT
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/db_xref-"GI:7108534"
/translation="MAGGGGMLRRLLRHRTETAVAIDSAFPLHALADHDVVPEDKF
/translation="MAGGGGMLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFP
/TRANSLAGECPATILAGECPATILAGECPATILAGESSSHKK
KOVDLNGSRKGRKPLAGPKAAVLPPRPPTKRKALEEPRATPPATRAKGA/GRDEXCKSSGCGGCFTTPNKFEDPSGILKNKARSGSSSLKPVVRAKGA/GRDEXCKSGCGCGC
GRSKKCIQGGETYTPNKFEDPSGILKNKARSGSSSLKPVVRAKGA/GRDEXCKSGDGCC
CPPLPSLPSEPQVNGKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPSGLWR
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WRCHFPTAAARPGTNLECKSCSADSTPTPGTPGEPAPTSGPRPAPGLAKVGDDSASHD
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/note="alternatively spl:
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Best Local Similarity 75.5%;
Matches 1240; Conservative
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                                    CCTTCTGAGCGAGCACCCTTCGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCCCG 1733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruan, Q.G., Wang, C.Y., Shi, J.D. and She, J.X. Expression and alternative splicing of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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ummalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
(bases 1 to 1921)
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                                                                                                                                                                                   SCCLQGRVQQNLSQPEVSRPPELPAETPILVGLRSASEKTRGPSRELKASSDAAVTYV
NLLAPHPAAPLLEPSALCPLLSAGNEGRPGPAPSARCSVCGDGTEVLRCAHCAAAFHW
RCHFTPAARFGTNLRCKSCSADSTPTPGTPGEAVPTSGPRPAPGLAKVGDDSASHDP
VLHRDDLESLLNEHSFOGILQMAIQSMSRPLAETPPFSS"

605 c 566 g 347 t
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                                                                                                                                                                                                                                                                                                                                              /product="autoimmune regulator"
/protein_id="AAF36462.1"
/bxref="GI:7108536"
/translation="MAGGDGMLRRLLRLHRTBIAVAIDSAFPLLHALADHDVVPEDKF
                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Aire"
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58. .1701
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                                                                                                      Score 923.8; DB 10;
Pred. No. 2.2e-153;
0; Mismatches 367;
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                                                                                                                                                                                                                                                                                                        Shimizu, N.
                                                                                                                                                                                                                                                                                                                                                     Nagamine, K., Peterson, P., Scott, H.S., Kudoh, J., Minosh Heino, M., Krohn, K.J.E., Lalioti, M.D., Mullis, P.E., Antonarakis, S.E., Kawasaki, K., Asakawa, S., Ito, F. and Positional cloning of the APECED gene Nat. Genet. 17 (4), 393-398 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB006685.1 GI:2696622
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                                                                                                                                                                                                                                                                                                                          (bases 1 to 1463)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens (isolate:Caucasian) 3-yr-old male thymus
                                                                                                                                                                                                                                                                                          Submission
/gene="APECED"
237. .1001
                                            /tissue_type="thymus"
/dev_stage="3-yr-old"
                                                                                /map="21q22.3"
/sex="male"
                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                  /chromosome="21"
                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                'isolate="Caucasian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa; Chordata; Craniata; Vertebrata;
                                 .1463
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                     TGGGCCATCCAGAGCATGGCCCGTCCGGGCGCCCCTTCCCCTGACCCCAGATGGCC
                                                                                                              AGCCCGCCCGCCTGGCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCT
CTGCACAGGGATGACCTGGAGTCCCTTCTGAGCGAGCACCCTTCGATGGCATCCTGCAG
                                                                                                                                                                        CGCTGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGTGCTGGCCCCC
                                                                   CTGCACAGGGATGACCTGGAGTCCCTTCTGAGCGAGCACACCTTCGATGGCATCCTGCAG
                                                                                                                                                                                                        GCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGGCCCGGGACGGGCCTG
                                                                                                                                                                                                                                                                                                              TCCTCGGCCCTGCACCCCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCT 1410
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945; Conserv
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/gene="APECED"
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/product="AIRE-3"
/protein_id="BAA23993.1"
/db_xref="GI:2696623"
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/note="autoimmune regulator-3"
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D; Mismatches 3;
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BASE COUNT
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AUTHORS
TITLE
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SOURCE
ORGANISM
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    Best Local Similarity
Matches 882; Conser
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Mammalla; Eutheria; Rodentia; Sciurognathi;
1 (bases 1 to 1637)
Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-FEB-1999) Pathology, Archer Road, Gainesville, FL 32610,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus autoimmune regulator (Aire) mRNA, spliced product 3a, complete cds. AF128122
AF128122.1 GI:7108545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruan, Q.G., Wang, C.Y., Shi, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulator gene (Aire)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Road, Gainesville, FL
Location/Qualifiers
1. .1637
                                                                                                     /translation="MAGGDGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF

GETLRLKEKEGCPQAFHALLSWLLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFF

KDVDLNGSRKGRKGLAGPKAAVLPPREPTKRKALEEPRATPPATLASKSVSSPGSHLK

TKPPKKPDGNLESQHLPLGMGIQTMAASVQRAVTVAEGDVPGTRGAVEGILIQQVFEK

GRSKKCIQVGGEFYTPNKFEDPSGNLKNKARSGSSLKFVVRAKGAQVTIPGRDEQKVG

QQCGVPPLPSLPSEPQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS

GLWRCSCCLQGRVQQNLSQPEVSRPPELPAETPDQSPLQILLCRLDSHARHTGRSCTH
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511 c 472 g
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                                                                                                                                                                                                                 /product="autoimmune regulator"
/protein_id="AAF36467.1"
/db_xref="GI:7108546"
                                                                                                                                                                                                                                                                        /gene="Aire"
/function="transcription factor"
/note="alternatively spliced pro
                                                                                                                                                                                                                                                                                                                           /gene="Aire"
58. .1287
                                                                                                                                                                                                                                                             /codon_start=1
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1. .1637
                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="B6"
                                                                                                                                                                                                                                                                                                                                                                                                                                    ∕organism≔"Mus musculus"
                 32.9%;
Score 737.6; DB 10
Pred. No. 1.5e-120;
0; Mismatches 219;
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                                                                  CCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGCTGCAGCTGCAGTGCCTCCAGTTCCCCCACTCTGCAGGAGATCCCCCAGTGGCCTCTGGAGATGCTCCTGCTGCTGCTCCCCACTGCAGGAGATCCCCCACTGCAGGAGATCCTCCCAGTGGCCTCTGCAGGAGATCCCCACTGCAGGAGATCCTCCCAGTGGCCTCCCA
           GGGCAGAGTCCAACAGAACCTGTCCCAGCCTGAGGTGTCCAGGCCCCCGGAGCTACCTGC
                                                                                                                                CCACGACGAGGTGAGCTCATCTGTTGTGACGGCTGTCCCCGGGCCTTCCACCTGGCTTG
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Search completed: February 14, 2003, 15:22:42 Job time : 5667.5 secs

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AAK68127 AAK77183	ABL32093 ABA15431	AAX26938	AAX26937	AAX26936	AAX58605	ID		SUMMARIES
Human immune/haema Human immune/haema	Human immune syste	cDNA encoding a hu	cDNA encoding a hu	cDNA encoding a hi	Human auto immuno p	Description		

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ABV59216	AAT11549	AAK77458	AAK68939	ABL69213	ABL68588	ABL66806	ABL62309	AAA55965	AAK73539	AAL03405	ABA15723	ABV25066	AAT11778	ABK91725	ABK72133	AAI62608	AAL03794	AAS09301	AAH51601	AAF24497	AAZ86967	AAK78433	AAK71542	AAS17705	AAL16277	AAL25120	ABL91800	AAS26741	AAD02697	ABL81253	AAK86282	ABQ88186	ABA20763	ABA20762	AAS98600
Human prostate exp	н		Human immune/haema	Prostate cancer re	Kidney cancer rela	a		_		_	_									Human PG-3 gene.	0			cDNA e	breast					ovarian	immune/haem	osteoblast	nervous	nervous sys	Human genomic DNA

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## ALIGNMENTS

RESULT 1 AAX58605

AAX58605 standard; cDNA; 2245

ВP

16-AUG-1999 (first entry)

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mutation
                                                                                                                              CDS
                                                           mutation
                                                                                                                                                                                Autoimmune polyendocrinopathy candidiasis ectodermal dystrophy; APECED; autoimmune polyglandular disease type 1; APGD1; AIRE; human; transcription factor; autoimmune disease; diagnosis;
                                                                                                mutation
                                                                                                                                                       Homo sapiens
                                                                                                                                                                           gene therapy; ss
                                                                                                                                                                                                                        Human autoimmune polyglandular disease type 1 (APGD1) cDNA.
                                              /note= "4-nucleotide insertion, results in replace(1090,CCTG)
/*tag= c
/note= "1-nucleotide insertion, results in
           replace(1284,A)
/*tag= d
                           /note= "4-nucleotide insertion, i
                                                                                              /product= "human_APGD1"
replace(1085,CCTG)
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ptide which co-segregates polyendocrinopathy candic
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256 aa ;
replace(358,T)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frameshift and truncated 478 aa protein" replace(889,T) /*tag= j
                                                                                                                                                                                                                                                                             /note= "Alu sequence overlapping with PFKL promoter starts at this position"
                                                                                                                                                                                                                                                                                                                                                                                                        /note= "silent polymorphism"
replace(801,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(1094,A)
/*tag= n
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                                                                                                                                                                                                                                                                                                                         note= "silent polymorphism"
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replace(1085..1097)
/*tag= f
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HEALTH INST.
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Perheentupa J, Yas
                          egates in mutated form - candidiasis ectodermal (
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Best Local Similarity
Matches 2245; Conserv
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                                                   GCTTTGGTACCGCCACCCAGACTCCCCACCAAGAGGAAGAGGCCTCAGAAGAGGCTCGAGCT
                                                                                              CCCAAAGATGTGGACCTCAGCCAGCCCCGGAAGGGGAGGAAGCCCCCGGGCCGTCCCCAAG
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                                         GCTTTGGTACCGCCACCCAGACTCCCCACCAAGAGGAAGGCCTCAGAAGAGGCTCGAGCT
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12-NOV-1997; 02-OCT-1997; 08-OCT-1997;

97EP-0119810. 97EP-0117154. 97EP-0117398.

02-OCT-1998; 15-APR-1999 W09918197-A2

98WO-EP06294

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WPI; 1999-287735/24 P-PSDB; AAY06073.

CC (see AAY5860-10), and off a 3'UTR extension PCR product. The encoded CC protein (see AAY66073) is a transcription factor or transcription-CC associated factor that may associate with vimentin fibres, perhaps CC as part of a docking mechanism regulating nuclear translocation. CC intermediate filaments. Mutated APGD1 polypeptides co-segregate With autoimmune polyendocrinopathy candidiasis ectodermal dystrophy CC (APECED). The invention provides vectors and host cells for preparation of APGD1 polypeptides. APECED-associated mutations CC preparation of APGD1 polypeptides. APECED-associated mutations CC (CCTG), normally found at position 1086-1089, at nucleotides CC (CCTG), normally found at position of an adenosine at position of CC 1284; an insertion of a cytosine at position 1365; a deletion of the cytosine at position 1309 or 1313; a cytosine to conclustion exchange at position 1909 or 1313; a cytosine to consistion 374; a guanosine to adenosine to guanosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1952; cand a cytosine to adenosine exchange at position 1962; cand a cytosine to adenosine exchange at position 1964. A claimed comethod for testing for a mutation in the APGD1 gene or for a cytosine to adenosine exchange at position 1964. A claimed method for the APGD1 polypeptide. APGD1 gene or for a cytosine to adenosine exchange at position and the apgon to for the diseas This is the nucleotide sequence of human autoimmune polyglandular disease type 1 (APGD1 or AIRE) cDNA. It is a composite of 2 clones, which were obtained from a human adult thymus cDNA library by PCR The encoded

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                                  23-SEP-1997;
                                               23-SEP-1998;
                                                             01-APR-1999
                                                                           WO9915559-A1
                                                                                                                                      APECED; autoimmune polyglandular
                                                                                                                                            disease;
                                                                                                                                                    Autoimmune regulator-1; AIR-1; immune maturation; immune response;
                                                                                                                                                                 cDNA encoding a human autoimmune regulator-1 (AIR-1) protein.
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Scott
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       Heino
                                  97FI-0003762
                                               98WO-FI00749
                     IMMUNOTECHNOLOGY
                                                                                                   Location/Qualifiers 137..1774
                                                                                       /product= "AIR-1"
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H,
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Claim

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Page 21-24;

Autoimmune

1999-244390/20 DB; AAY01712.

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to immune maturation and regulation of immune response towards self and nonself. They can be used particularly in the diagnosi and treatment of autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECED) (also known as autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyglandular syndrome type I (APS I)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes an autoimmune regulator-1 (AIR-1) protein. The AIR polypeptides and polynucleotides can be used in methods for the diagnosis and treatment of diseases related
          GGAGCCCGAGGGGCCGTGGAGGGGATCCTCATCCAGCAGGTGTTTGAGTCAGGCGGCTCC
                                      ATTCAGACCATGTCAGCTTCAGTCCAGAGAGCTGTGGCCATGTCCTCCGGGGACGTCCCG
                                                                            AAGCCCCCCAAGAAGCCGGAGAGCAGCGGCAGCAGCAGCGCCTTCCACTCGGGAACGGG
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Query Match Best Local Matches

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89.9%; nilarity 100.0%; Conservative 0

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Sequence 2036 BP;

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                                                                                                                              The present sequence encodes an autoimmune regulator-2 (AIR-2) protein. The AIR polypeptides and polynucleotides can be used in methods for the diagnosis and treatment of diseases related to immune maturation and regulation of immune response towards self and nonself. They can be used particularly in the diagnosis and treatment of autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECED) (also known as autoimmune
                                                                                               Sequence 1545 BP; 261 A; 485 C; 508
                                                                                                                     ectodermal dystrophy (APECED) (also known polyglandular syndrome type I (APS I)).
                                                                                                                                                                                                                               Claim 4; Page 27-29; 59pp; English.
Autoimmune regulator 1 (AIR1) DNA sequence
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Peterson P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding a human autoimmune regulator-2 (AIR-2) protein.
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                                                               Similarity
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237.1283
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99.7%;
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Pred. No. 3.9e-
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                                           TTCTCTACTCTGGAAGTCCCCGGGAGCCTCTCCTTGCCTGGTGACCTACTAAAAATATAA
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RESULT 4
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Matches 1249; Conserv
                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of murine AIRE cDNA. Murine AIRE is the homologue of the human AIRE (or autoimmune polyglandular disease type 1, APGD1) gene (see AAX58605). The overall nucleotide sequence identity between the mouse AIRE coding sequence and that of the human is 76.67%. The mAIRE gene was localised to chromosome 10. Human mutated APGD1 co-segregates with autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECED). The murine homologue may be used to develop an animal model for APECED, to examine the events that lead to the development of APECED and possibly to develop agents for preventing and/or treating this
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02-OCT-1997;
08-OCT-1997;
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                                                                                                                                                                                                                                                                                             Sequence 1656 BP; 344 A; 532
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                         GTCCTGGCTCCTGACCCGGGACAGTGGGGCCATCCTGGATTTCTGGAGGATTCTCTTTAA
                                          GTCCTGGCTGCTGACCCAGGACTCCACAGCCATCCTGGACTTCTGGAGGGTGCTGTTCAA
                                                                              CCAGGAGACGCTCCGTCTGAAGGAGAGGAAGGCTGCCCCCAGGCCTTCCACGCCCTGCT
                                                                                          TCAGGAGACGCTTCATCTGAAGGAAAAGGAGGCCTGCCCCCAGGCCTTCCACGCCCTCCT
                                                                                                                                              CAGCGCCTTCCCACTGCTGCACGCGCTGGCTGACCACGACGTGGTCCCCGAGGACAAGTT 248
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                                                                                                                                  CAGTGCCTTTCCGCTGCATGCTCTAGCCGACCACGACGTGGTCCCTGAGGACAAGTT
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97EP-0117154.
97EP-0117398.
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76.0%;
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Perheentupa J, Yas
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Pred. No. 3.
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                                                                                                                                                                                                                                      ore 964.2; DB 20; ed. No. 3.3e-179; Mismatches 373;
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                   to immune maturation and regulation of immune response towards self and nonself. They can be used particularly in the diagnosis and treatment of autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECED) (also known as autoimmune polyglandular syndrome type I (APS I)).
                                                                                                                         protein. The AIR polypeptides and polynucleotides can be used in methods for the diagnosis and treatment of diseases related to immune maturation and regulation of immune.
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Peterson P, Scott H,
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                                                                                                                                                                                                                                                               Claim 4; Page 31-32; 59pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 945; Conserv
                                                                                                                                        TTCTCTACTCTGGAAGTCCCCGGGAGCCTCTCCTTGCCTGGTGACCTACTAAAAATATAA
                                                          CAGCTCTGTGTTTCTGGGGACACCAGCCATCATGTGCCTGGAAATTAAAACCCTGCCCCAC
                                                                                                      GCCGGCCGGCTGGGATCAAGAAGGGGACAGCGCCACCTCTTGTCAGTGCTCGGCTGTAAA
TTCTCTACTCTGGAAGTCCCCGGGAGCCTCTCCTTGCCTGGTGACCTACTAAAAATATAA
                                             CAGCTCTGTGTTTCTGGGGACACCAGCCATCATGTGCCTGGAAATTAAACCCTGCCCCAC
                                                                                           GCCGGCCGGCTGGGATCAAGAAGGGGACAGCGCCACCTCTTGTCAGTGCTCGGCTGTAAA
                                                                                                                                                                                       TGGGCCATCCAGAGCATGGCCCGTCCGGCCGCCCCTTCCCCTCCTGACCCCAGATGGCC
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                                                                                                                                                                                                                                    CTGCACAGGGATGACCTGGAGTCCCTTCTGAGCGAGCACCCTTCGATGGCATCCTGCAG
                                                                                                                                                                                                                                                                                  CGCTGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGTGCTGGCCCCC
                                                                                                                                                                                                                                                                                                                                                                                          GCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTG
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                                                                                                                                                                                                                                                                                                                                 CGCTGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGGTGCTGGCCCCC
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Pred. No. 3.7
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1.7e-157;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
Claim 1; SEQ ID NO 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune system associated gene SEQ ID NO:
                                                                                                                                                             61
                                                                                                                                                                                                                                                                         μ
                                                                                                                    GCTGCCAGTGTCCCGGGACCCACCGCGTCCGCCCCAGCCCCGGGTCCCCCGCGCCCCACCCC
                                                                                    ACTACCAATATCCCGAAACCCACCGCGCTCCGCCCCAACCCCGAATCCCCCGCGCCCACCCC
                                                                                                                                                                                                                                                     CGGGCGCACAGCCGGGGGGGGGGGCCCACAGCCCGGCCGGGGACCCGAGGCCAAGCGAGGG
                                                                                                                                                                                                CGAACGCACAACCGACGCGAAAACCCCCACAACCCCGCGGAAACCCGAAACCAAAACGAAAA
                                                                                                                                                                                                                                                                                                                                                        Similarity
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                    1882 A; 309 C; 3154 G;
                                                                                                                                                                                                                                                                                                                                                7.5%;
79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
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Pred. No. 1.4e
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ABA15431/c
ABA15431/c
ABA15431;
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AC ABA15431;
XX
DT 23-JAN-2002 (first entry)
XX
DT 23-JAN-2002 (first entry)
XX
DT 23-JAN-2002 (first entry)
XX
Human nervous system related polynumical entry
XX
Human noctropic; neuroprotective; introduced entry
XX
Human; noctropic; neuroprotective; introduced entry
XX
Antiparkinsonian; antisickling; antidiabetic; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4629
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2000US-0229287. 2000US-0229343.

01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000

2000US-0229513. 2000US-0230437. 2000US-0230438. 2000US-0231242. 2000US-0231242. 2000US-0231243.

2000US-0231244. 2000US-0231413. 2000US-0231414.

2000US-0232080. 2000US-0232081.

2000US-0232397

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Best Local 9
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17-NOV-2000;
17-NOV-2000;
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01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
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06-DEC-2000
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                            marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                            1996
                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast in the diagnosis treatment and prevention of: (b) cancer, bone, bone marrow breast castrointestinal tract liver lives are recentled.
                                                             1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancers and metastases
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17-NOV-2000;
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 7762; 1701pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 - NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000;
                 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA
                                                          GGGAGGCTGAGGCAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGTCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-541565/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME
                                                                                                                                        Similarity
                                                                                                                                                                                      25012 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US - 0249212

2000US - 0249213

2000US - 0249215

2000US - 0249216

2000US - 0249217

2000US - 0249217

2000US - 0249244

2000US - 0249245

2000US - 0249245

2000US - 0249265

2000US - 0249265

2000US - 0249297

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2000US - 0251130

2000US - 02511856

2000US - 02511856

2000US - 02511856

2000US - 02511859

2000US - 02511899

2000US - 02511899

2000US - 0251097

2000US - 0251097

2000US - 0251989

2000US - 0251989

2000US - 0251997

2000US - 0251997
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SC,
                                                                                                                                                                                      6932 A; 4835 C;
                                                                                                                                      6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3224 human nervous system antigen polypeptides, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben
                                                                                                                        0;
                                                                                                                      Score 155.2;
Pred. No. 4.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MS
                                                                                                                                                                                    5560 G;
                                                                                                                                     4.7e-21
                                                                                                                                                       ₽B
                                                                                                                                                                                      7685 T; 0 other;
                                                                                                                      28;
                                                                                                                                                     22;
                                                                                                                        Indels
                                                                                                                                                     Length 25012;
                                                                                                                                                                                                                                                                                                                                                                                                         e.g. breast
                                                                                                                        0;
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2000US

S-0236367. S-0236368. S-0236369. S-0236370. S-0236802. S-0236802.

2000US-0237038. 2000US-0237039. 2000US-0237040. 2000US-0239935. 2000US-0239937.

S-0240960. S-0241785. S-0241786. S-0241787.

25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

14-SEP-2000; 21-SEP-2000; 21-SEP-2000;

29-SEP-2000 29-SEP-2000 29-SEP-2000 20-CCT-2000 20-CCT-2000 20-CCT-2000 21-CCT-2000 21-CCT-2000 21-CCT-2000 20-CCT-2000 20-NOV-2000 20-NO

2000US - 0241808
2000US - 0241809
2000US - 0241829
2000US - 024221
2000US - 0246476
2000US - 0246475
2000US - 0246476
2000US - 0246476
2000US - 0246477
2000US - 0246477
2000US - 0246478
2000US - 0246524
2000US - 0246524
2000US - 0246526

Gaps

0;

2115

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RESULT 8
AAK68127
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                24-FEB-2000)
02-MAR-2000)
16-MAR-2000)
18-MAR-2000)
19-MAY-2000)
19-MAY-2000)
28-JUN-2000)
20-JUN-2000)
11-JUL-2000)
11-JUL-2000)
11-JUL-2000)
11-JUL-2000)
14-MUG-2000)
14-AUG-2000)
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04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK68127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK68127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune; haematopoietic; immune/haematopoietic antigen;
atic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                2000US-0186350
2000US-019874
2000US-0198123
2000US-0209451
2000US-0215135
2000US-0216647
2000US-0216647
2000US-0216880
2000US-0217487
2000US-0217487
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2000US-0225214
2000US-0225214
2000US-0225266
2000US-0225275
2000US-0225275
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2000US-02258270
2000US-02258270
2000US-02258266
2000US-02258270
2000US-02228824
2000US-02228824
2000US-0229343
2000US-0229345
2000US-0229345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0179065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0184664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
      06-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
14-SEP-2000
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14-SEP-2000
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14-SEP-2000
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21-SEP-2000
21-SEP-2000
21-SEP-2000
21-SEP-2000
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26-SEP-2000
27-SEP-2000
29-SEP-2000
20-CCT-2000
20-CCT
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2000US-0241786
2000US-024677
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2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
2000US-0249211
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2000US-0231242.

2000US-0231243.

2000US-0231244.

2000US-0231414.

2000US-0231414.

2000US-0232080.

2000US-0232080.
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                                                                                                                                                                                                                                                                                                         ARK54951 to ARK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cactivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat discorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC to AAK87694 represent human immune/haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 cc represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                              Query Match 6.9%;
Best Local Similarity 81.0%;
Matches 179; Conservative
                                                                                                                                                                          1785
                                                                                                                                                                                                      1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
                                                                                                                   1845
                                                                                                                                               2056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC
05-DEC
05-DEC
06-DEC
08-DEC
08-DEC
08-DEC
08-DEC
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 22939; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DEC-2000;
                                                                    TTGCGCCACTGCACTCCAGTCTGGTCGGCAGAGAGTGAGACTCCGTCTCAAAAACAAAACA
                                                                                                                          GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGGTGAGAC
                                                                                                                                                                  AAAAAAAAAGAAAAGAAAAGAAAAAAGGCCAATCGTGTTT 2005
                          AAAAAACCACATAACATAAATTTATCATCTCGACCACTTTT 2216
                                                                                                             2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -2000;
                                                                                                                                                                                                                                                                                        5540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0249244.
2000US-0249245.
2000US-0249265.
2000US-0249265.
2000US-0249397.
2000US-0249300.
2000US-0250160.
2000US-0251030.
2000US-0251030.
2000US-02511988.
2000US-0251868.
2000US-0251868.
2000US-0251868.
2000US-0251868.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251899.
2000US-0254097.
                                                                                                                                                                                                                                                                                     BP; 1875 A; 1111 C; 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                             Score 153.8; DB 22; Length 5540;
Pred. No. 7.2e-21;
0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MS
                                                                                                                                                                                                                                                                                    G; 1402 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides and
                                                                                                                                                                                                                           Gaps
                                                                                  2175
                                                                                                                                         2115
                                                                                                              1904
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RESULT 9
AAK77183/c
ID AAK77183 standard; DNA; 2648
 18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

30-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000
                                                                                                                                                                                                          14 - AUG - 2000)
                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                                                26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                         11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; gene therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK77183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune; haematopoietic; immune/haematopoietic antigen; cancer;
20000S-0229344
2000US-0229345
2000US-022959
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2000US-0232080
2000US-0232081
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2000US-0218290.
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                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0214886
2000US-0215135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000us-0179065
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5-0216880.
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14-SEP-2000; 14-SEP-2000;

2000US-0232401 2000US-0233063

2000US-0231968. 2000US-0232397. 2000US-0232398.

2000US-0233064 2000US-0233065 2000US-0234223 2000US-0234274 2000US-0234998 2000US-0234998 2000US-0235834 2000US-0235834 2000US-0235836 2000US-0235836 2000US-0236368 2000US-0236368 2000US-0236369 2000US-0236369 2000US-0236370 2000US-0236370 2000US-02363737

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RESULT 10
AAS98600
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                                                                                                                                                                                                                                                  DЪ
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                                                                                                                                                                                                                                                                                                                                                                CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC to AAK87694 represent human immune/haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 185
                                                                                                     2176
                                                                                                                                                                                          1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
11-DEC-2000;
  AAS98600
                                                                                                                                                              2116
                                                                                                                                                                                                                       2056
                                                                                                                                                                                                                                                  1121
                                                                                                                                                                                                                                                                              1996
                                                                                                                                                                                                                                                                                                                                                         Sequence 2648 BP; 563 A; 750 C; 744 G; 591 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                   941 ТААААСААААААСААААСААААААААААААААААААССТТААТСТААТGACGCATCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ( HUMA - )
                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                          AAAAAACCACATAACATAAATTTATCATCTCGACCACTTTTCAGTTCAGTGGCATTCACA
                                                                                                                                                                                 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGGTGAGA
                                                                                                                                                                                                                                          CTACTAAAAATACAAAAATTAGCTGGGTGGTGGTGGGTGCCTGTAATCCCAGCTACTT
                                                                                                                                                                                                                                                           2001-483426/52.
                                                                                                                                                                                                                                                                                                        185;
  standard;
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                                                                                                                                                                                                                                                                                                        Conservative
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2000US-0251030.
2000US-025198.
2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0251869.
2000US-0251989.
2000US-0251989.
2000US-0251989.
2000US-0251989.
2000US-0251989.
2000US-0251989.
 DNA; 140036
                                                                                                                                                                                                                                                                                                                 6.8%;
77.1%;
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Pred. No. 1.5e-20;
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2000US-0241826. 2000US-0244617. 2000US-0241808. 2000US-0241809.

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2000US-0237038 2000US-0237039

2000US-0240960. 2000US-0241221. 2000US-0241785. 2000US-0241786. 2000US-0241787.

2000US-0237040. 2000US-0239935. 2000US-0239937.

08-NOV-2000 17-NOV-2000 17-NOV-2000

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2000US-0249245
2000US-0249297
2000US-0249299
2000US-0249299

17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

12-MAR-2002 AAS98600;

(first entry)

17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

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                                                                                                                                                                                                                                                                                              CC receptor substrate (IRS) family, and signal transducer and activator of CC transcription (STAT) transcription factors, to receptors that interact CC with and phosphorylate the proteins and STAT transcription factors, CC the nucleic acid encoding PHIP (nPHIP), a nucleic acid which binds to CC nPHIP or regions of it, analogues, fragments or allelic variants of PHIP CC or nPHIP, a nucleic acid sequence having substantial sequence identity or Sequence similarity with a nucleic acid sequence fully defined CC mean neuronal differentiation-related protein (NDRP) nucleic acid conduction sequence or its exons as given in the specification, expression CC vectors and host cells expressing the nucleic acids, anti-PHP antibodies, and transgenic animal not already expressing PHIP. The nucleic acids, proteins and antibodies are useful for diagnosis and treatment of CC acids, proteins and antibodies are useful for diagnosis and treatment of CC acids, retinopathy, nephropathy, artherosclerosis, peripheral CC arterial disease) or cancer (e.g. adenocarcinoma, leukaemia, breast CC cancer, prostate cancer, colon cancer, ovarian cancer and many others CC cloner, in the specification, autoimune disease, inflammation and CC concer, in the specification, autoimune disease.
                                                                                                                                    Query Match
Best Local
                                                                                                                Matches
                                        1934
  2056
                                                                                                                                                                                                                                            given in the specification), autoimmune disease, inflammation and immunodeficiency. The protein is also useful for discovering or testing compounds which may be either enhancers or inhibitors of PHIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHIP; Plecketrin homology domain-interacting protein; NDRP; ds; neuronal differentiation-related protein; insulin receptor substrate; IRS; signal transducer and activator of transcription; STAT; transgenic animal; diabetes mellitus type 2; hyperglycaemia; myotonic muscular dystrophy; acanthosis; nigricans; retinopathy; nephropathy; artherosclerosis; peripheral arterial disease; cancer; nephropathy; artherosclerosis; peripheral arterial disease; colon cancer;
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated Pleckstrin homology domain interacting protein (PHIP) that recruits proteins of the insuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 99-133; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and activator of transcription factors to their receptors, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Pleckstrin homology domain interacting protein recruiting proteins of insulin receptor substrate family, and signal transducer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rozakis-Adcock M,
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                                GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROZAKIS-ADCOCK M. FARHANG-FALLAH J.
                                                                                                                                    Similarity
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                                                                                                                                                                                          140036 BP; 48500 A;
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                                                                                                                Conservative
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                                                                                                                                                                                                                            present sequence is genomic DNA encoding PHIP and
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26-JUL-2000;
14-AUG-2000;
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07-JUL-2000;
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16-MAR-2000;
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28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; neuroprotective; cytostatic; immunosuppressive; antiinflammatory; anti-HIV; antiparkinsonian; antisickling; antianaemic; ar
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19-MAY-2000;
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2000US-0225213.
2000US-0225214.
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2000US-0198123.
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2000US-0220963
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2000US-0229509 2000US-0229513 2000US-0230437 2000US-0231438 2000US-0231242 2000US-0231243 2000US-0231243 2000US-0231241 2000US-0231414 2000US-0231414 2000US-0232080 2000US-0232080

2000US-0229344

14-SEP-2000;

2000US-0232398. 2000US-0232399. 2000US-0232400.

2000US-0231968 2000US-0232397

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                                                                                                                                                                                                                                                                                                                               The invention relates to novel genes (ABA11004-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast can ovarian cancer and other cancers of the adrenal gland, bone, bone CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative (c) cardiovascular disorders such as myocardial ischaemias; CC epilepsy; and (f) infectious diseases e.g. cerebral anoxia and CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly xxx
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2000US-0251479.
2000US-0251856.
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                                                                                                                                                                                                                             Score 151.6; DB 22; Pred. No. 2.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Listing; English.
                                                                                                                                                                                     2.4e-20;
39;
                                                                                                                                                                                                                                                                                            6457 T; 0 other;
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                               Length 26427;
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                                                                                                                                                                                             Gaps
                                                                                                 4431
                                                                                                                                              2055
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14-SEP-2000
14-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
02-OCT-2000
01-NOV-2000

2000US-0234274 2000US-0234274 2000US-0234274 2000US-0234997 2000US-0234998 2000US-0235834 2000US-0235834 2000US-0235836 2000US-0235836 2000US-0236327 2000US-0236368 2000US-0236368 2000US-0236369 2000US-0236369

08-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
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17-NOV-2000

2000US-0249211

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RESULT 12
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      07-JUN-2000
28-JUN-2000
30-JUN-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
14-JUL-2000
14-JUL-2000
14-AUG-2000
18-AUG-2000
23-AUG-2000
23-AUG-2000
30-AUG-2000
30-AUG-2000
30-AUG-2000
30-AUG-2000
30-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antistckling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4311
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07
28
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antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
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      2000US-0186350
2000US-019974
2000US-0199123
2000US-0204515
2000US-0214886
2000US-0216847
2000US-0216847
2000US-0216880
2000US-0217487
2000US-0217487
2000US-0217487
2000US-0217487
2000US-0218290
2000US-0224518
2000US-0224518
2000US-0225267
2000US-0225267
2000US-0225267
2000US-0225268
2000US-0225268
2000US-0225268
2000US-0225268
2000US-0225268
2000US-0225268
2000US-02252688
2000US-02256881
2000US-02258888
2000US-02238924
2000US-02238924
2000US-02238924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US01334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180628
2000US-0184664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system related polynucleotide SEQ ID NO 13094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; nephrotropic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26427
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    25-SEP-2000

26-SEP-2000

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29-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

20-CCT-2000

02-CCT-2000

03-CCT-2000

03-CCT-2000

04-NOV-2000

06-NOV-2000

08-NOV-2000

08-NO
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14-SEP-
14-SEP-
21-SEP-
21-SEP-
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12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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08-SEP-2000;
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-2000;
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2000US-0229344
2000US-0229503
2000US-0229503
2000US-0229503
2000US-0231243
2000US-02311243
2000US-02311414
2000US-02311414
2000US-02313063
2000US-0233396
2000US-0233396
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2000US-02354844
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2000US-02354844
2000US-02354833
2000US-0236367
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                                                                                                         1996 CTACTAAAAATATAAAAATTAGCTGGGTGTGGGTGGGTGCCTGTAATCCCCAGCTACAT
                                                                                                                                                                                                                                                                The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer useful and ovarian cancer and other cancers of the adrenal gland, bone, bone (b) immune disorders e.g. Addison's disease, allergies, autoimmune (b) autoimmune thyroiditis, diabetes mellitus, Crohn's colitis; (c) cardiovascular disorders such as myocardial ischaemias, entities (c) cardiovascular disorders such as myocardial ischaemias, epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                          Sequence 26427 BP;
                                                                                                                                                                                                                                           printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14078-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 13094; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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08-DEC-2000;
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08-DEC-2000;
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01-DEC-2000;
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17-NOV-2000;
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                                                                                                                                                                   Local Similarity
TTGCGCCACTGCACTCCAGTCTGGGTCGGCAAGAGTGAGACTCCGTCTCAAAAACAAAACA
                                                    GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115
                                        GGGAGGCTGAGGCAGGAGTTGCTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCCGAGA
                                                                                           CTACTAAAAATACAAAAATTAGCTGGGTGTGGTGGTGCATGCCTGTAATCTCAGCTACTC 4431
                                                                                                                                                        186;
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                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and metastases
                                                                                                                                                                                                                                    at
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash
                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0251869.
2000US-0251989.
2000US-0251990.
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2000US-0251988.
2000US-0256719.
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2000US-0249215.
2000US-0249216.
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2000US-0251868
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                                                                                                                                                                                                      5634 A; 7262 C;
                                                                                                                                                                 6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3224 human
diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben
                                                                                                                                                    0,
                                                                                                                                                                Pred.
                                                                                                                                                                 Score 151.6;
Pred. No. 2.4
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                                                                                                                                                  ed. No. 2.4e
Mismatches
                                                                                                                                                                                                     7074 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nervous system antigen polypeptides, and/or treating nervous system
                                                                                                                                                 2.4e-20;
hes 39;
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                                                                                                                                                                         DB 22;
                                                                                                                                                                                                   6457 T; 0 other;
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1;

Gaps

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2055

2175 4371

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1996 CTACTAAAAATATAAAAATTAGCTGGGTGGTGGTGGTGGTGCCTGTAATCCCAGCTACAT 2055

Matches Query Match

Local Sim hes 169;

Similarity

6.8%; 85.4%;

Score 151.6; DB 24; Pred. No. 3.1e-20;

24;

Indels Length

0; Gaps

0;

Conservative

0,

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RESULT 13
ABQ88186
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                           monitoring the progression of bone tissue deposition. Specific conditions include postmenopausal osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drug-induced abnormalities in bone formation or bone loss, conditions that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome or fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated CDNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire, wipo.int/pub/published_pct_sequences.
       Sequence
                                                                                                                                                                                                         osteoblast formation or osteoporosis; or
                                                                                                                                                                                        (c) treating or monitoring treatment of the conditions cited in (b), or
                                                                                                                                                                                                                   (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
                                                                                                                                                                                                                                             osteoblasts, or
                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                   Use of genes and their expression profiles associated with differentiation for screening modulators bone formation, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ji D,
                                                                                                                                                                                                                                                                                      The invention
                                                                                                                                                                                                                                                                                                                                                 process
                                                                                                                                                                                                                                                                                                                                                         or treating e.g. osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-557663/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2000;
24-APR-2001;
                                                                                                                                                                                                                                                        (a) screening modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mertz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENE LOGIC INC. (PROC ) PROCTER & GAMBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2001; 2001WO-US48276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; osteoblast; stem cell differentiation; bone tissue deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoporosis; osteopathic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human osteoblast differentiation related cDNA SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAAAAAAAAAAGAGTTACTTTTAATTCCTACCTCTTCTACTTT 4266
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169739 BP; 49809 A; 35660 C; 35715 G; 48555 T; 0 other;
                                                                                                                                                                                                                                                                                                                   SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-255882P
2001US-285691P
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                                                                                                                                                                                                                                                                                   relates to genes and
                                                                                                                                                                                                                                       odulators of precursor stem cell differentiation into bone tissue deposition;
                                                                                                                                                                                                                                                                                                                NO 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA; 169739
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cook JS,
                                                                                                                                                                                                                                                                                                          78pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                   their
                                                                                                                                                                                                                                                                                                                                                       markers for the differentiation
                                                                                                                                                                                                                                                                              expression profiles are used
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                                                                                                                                                                                                                                                                                                                                                                th osteoblast for diagnosing
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11 - JUL - 2000; 16 - APR - 2000; 17 - MAR - 2000; 18 - APR - 2000; 19 - APR - 2000; 19 - JUL - 2000; 10 - JUL - 2000; 11 - JUL - 2000; 12 - JUL - 2000; 14 - AUG - 2000; 15 - AUG - 2000; 16 - AUG - 2000; 17 - AUG - 2000; 18 - AUG - 2000; 19 - AUG - 2000; 10 - AUG - 2000; 11 - AUG - 2000; 11 - AUG - 2000; 12 - AUG - 2000; 13 - AUG - 2000; 22 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 21 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 24 - AUG - 2000; 25 - AUG - 2000; 27 - AUG - 2000; 28 - AUG - 2000; 29 - AUG - 2000; 20 - AUG - 2000; 20 - AUG - 2000; 21 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 24 - AUG - 2000; 27 - AUG - 2000; 28 - AUG - 2000; 29 - AUG - 2000; 20 - AUG - 2000; 20 - AUG - 2000; 21 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 24 - AUG - 2000; 25 - AUG - 2000; 27 - AUG - 2000; 28 - AUG - 2000; 29 - AUG - 2000; 20 - AUG - 2000; 21 - AUG - 2000; 21 - AUG - 2000; 22 - AUG - 2000; 23 - AUG - 2000; 24 - AUG - 2	Db 9972 CTACCGAAAATATAAAAATTAGCCGGGTGTGGGTGGAGAGTGTCTGTAATCCCAGCTACTT 100031  Qy 2056 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTTGAA
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                                                                                                                                                                                                                                           CC amino acid sequences given in AAM82170 to AAM81921. (1) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (1) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC expression by rectifying mutations or deletions in a patient's genome CC expression by rectifying moduction of the proteins or to CC polynucleotides may be used to production of 10. Additionally, (1) CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (1) proteins and polynucleotides may be used to produce the secreted (1), by inserting CC cancers and cancer metastases of haematopoietic-related diseases, especially to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM64703 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                          Matches
                                                                                                                                                                                            Query Match
Best Local
                                                          35959
                                                                                                   35899 CTACTAAAAATACAAAAATTAGTTGGGCGTGGCAGGTGCCTGTAGTCCCAGCTACTT 35958
                                                                                       2056
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2000
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08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK54951 to AAK64702 encode the human immune/haematopoietic antigen amino acid sequences given in AAM82170 to AAM91921. (I) have cytosta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 41094; 3071pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen useful for preventing, diagnosing and/or treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483426/52.
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11-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-2001;
                                                                                                                                                                            Local Similarity
les 171; Conserv
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TTGCGCCACTGCACTCCAGTCTGGTCGGCAAGAGTGAGACTCCGTCTCAAAAACAAAACA 2175
                                              GGGAGGCTAAGGCAGGAGAATTGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGA
                                                               GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTTGCAGGTTGCAGTGAGCTGAGA 2115
                                                                                                                                                                                                                       65854 BP; 18519 A; 14498 C; 14223 G; 18614 T; 0 other;
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2000US-0254097.
2001US-0259678.
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2000US-0251479
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2000US-0251988
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2000US-0249297
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83.8%;
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                                                                                                                                                                       0;
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Pred. No. 3.3e-20;
); Mismatches 33
                                                                                                                                                                                           DB_22; Length 65854;
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                                                                                                                                                                 0;
                                                                                                                                                              Gaps
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Matches Query Match Best Local 9

188;

Conservative

0;

Local Similarity

6.7%; 75.2%; A; 96 C;

Score 150.8; Pred. No. 1.9e 0; Mismatches

1.9e-20; 62;

0;

Gaps

0;

DB 24; Length 462; Indels

Sequence

462

BP; 120

84 G;

162 T; 0 other;

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CC ABLB7934, (III) encoding (II) having a sequence (S2), a T cell

(C) population of (II), or antigen presenting cells that express (II).

(C) (II) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological contacting a biological sample preferably serum or ovarian tissue. The method comprises (C) contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to gradient, where the amount of polynucleotide bybridising to (IV) is cells (C) patient, where the amount of polynucleotide bybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising CC specific for an ovarian tumour protein comprising contacting T cells (C) specific for an ovarian tumour protein comprising contacting T cells (C) with (III) or (II), (III) is useful in design and preparation of cand proteins in tumour cells; and to isolate a full length gene from a contacting techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
ABL81253/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЬ
                                                                                                                                                                                                                                                                                                          The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID 4231; 489pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36079 AAAAAAAAATTCTCATGAAATTA 36102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAY-2001; 2001WO-US17756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000; 2000US-207484P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200192581-A2
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Result
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Listing first 45 summaries
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        150.8
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Gapop 10.0 , Gapext 1.0
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2245
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       /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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US-09-764-864-1715
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Sequence 3, Appli
Sequence 1892, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 314, App
                                                              Sequence 58, Appl
Sequence 160, Appli
Sequence 2, Appli
Sequence 2116, Ap
Sequence 2116, Ap
Sequence 332, App
Sequence 331, App
Sequence 331, App
Sequence 1, Appli
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Sequence 1715, Ap
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45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
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6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4
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9	10	10	10	9	10	10	10	10	10	10	10	10	10	10	10	10	10	9	9	9	9	10	10	10	10
US-10-161-510-1	US-09-764-860-797	US-09-764-860-798	US-09-818-656A-3	US-10-216-441-3	US-09-764-847-1966	US-09-764-877-3063	US-09-764-864-1692	US-09-939-581A-3	US-09-867-701-7179	US-09-764-869-2292	US-09-880-107-2798	US-09-835-081-3	US-09-764-877-2544	US-09-764-877-2536	US-09-764-860-777	US-09-727-770-3	US-09-764-853-894	US-09-989-442-159	US-09-860-670-150	US-09-764-868-1375	US-09-764-868-1374	US-09-820-905-3	US-09-729-920-3	US-09-751-877-1	US-09-764-847-1965
Sequence 1, Appli	Sequence 797, App	Sequence 798, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 1966, Ap	Sequence 3063, Ap	Sequence 1692, Ap	Sequence 3, Appli	Sequence 7179, Ap	Sequence 2292, Ap	Sequence 2798, Ap	Sequence 3, Appli	Sequence 2544, Ap	2536	Sequence 777, App	Sequence 3, Appli	Sequence 894, App		Sequence 150, App	Sequence 1375, Ap	Sequence 1374, Ap	ω	Sequence 3, Appli	1, App	Sequence 1965, Ap

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## ALIGNMENTS

US-09-867-701-4231/c

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CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4231
LENGTH: 462
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-4231
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                                                                                                                                                                                                                                                                                                                                                                             Matches 188;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.7%;
Best Local Similarity 75.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
                                                                                   2176
                                                                                                                      1996 CTACTAAAAATATAAAAATTAGCTGGGTGGTGGTGGTGGCCTGTAATCCCCAGCTACAT 2055
                                                                                                                                                                                                                             2056 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTTGGAGGTTGCAGTGAGCTTGAGA 2115
2236 TCTCATGTAA 2245
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                                                                 AAAAAACCACATAACATAAATTTATCATCTCGACCACTTTTCAGTTCAGTGGGCATTCACA 2235
                                       AAAAAAAAAAAAGCTTATTTCTAAGATATCATCTATTCTCCAATTTTGTACTTTTATGA 214
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; ORGANISM: Homo sapiens
US-09-764-864-1715
                                      Query Match
Best Local Similarity
Matches 176; Conserv
                                                                                                                      SEQ ID NO 58
LENGTH: 3535
TYPE: DNA
ORGANISM: Homo sapien
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Sequence 1715, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 58, Application US/09989920 Patent No. US20020172957A1
                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0291
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                                                                                                                                                                                             SOFTWARE:
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CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
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Chen, Sei-Yu
                                           Conservative
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Pred. No. 3.5
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                                                                         PRIOR APPLICATION NUMBER: USO PRIOR FILING DATE: 2001-01-17
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PRIOR APPLICATION NUMBER: US01/01349
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PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,892
PRIOR FILING DATE: 2001-01-17
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      FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01348
                                                                                       APPLICATION NUMBER: US01/01239
                                                        APPLICATION NUMBER:
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FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01334
FILING DATE: 2001-01-17
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FILING DATE: 2001-01-17
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APPLICATION NUMBER: US01/01329
FILING DATE: 2001-01-17
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SOFTWARE: Patentin Ver. 2
SEO ID NO 160
LENGTH: 1186
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (347)
OTHER INFORMATION: n e
NAME/KEY: SITE
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PRIOR FILING DATE: 2000-06-07
NUMBER OF SEA TO
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OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (349)
OTHER INFORMATION: n e
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LOCATION: (354)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
LOCATION: (355)
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OTHER INFORMATION: n equals a,t,g, or c
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NAME/KEY: SITE
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OTHER INFORMATION:
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FILING DATE: 2001-01-17
ADDITION STATE: 2001-01-17
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APPLICATION NUMBER: 09/764,896
FILING DATE: 2001-01-17
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APPLICATION NUMBER: 09/764,856
FILING DATE: 2001-01-17
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OTHER INFORMATION: (
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OTHER INFORMATION: 1
NAME/KEY: SITE
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LOCATION: (357)
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LOCATION: (368)
OTHER INFORMATION: n
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NAME/KEY: SITE
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LOCATION: (374)
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LOCATION: (362)
OTHER INFORMATION: n
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OTHER INFORMATION: n equals a,t,g,
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SEQ ID NO 2
TENGTH: 21278
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ESSIOUX, Laurent
TITLE OF INVENTION: Genes, proteins and bi
FILE REFERENCE: GENSET.045AUS
CURRENT FILING DATE: 1999-10-12
CURRENT APPLICATION NUMBER: US/09/416,384A
PRIOR APPLICATION NUMBER: 60/106,457
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-
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                                                        OTHER INFORMATION: 99-16063.pu
                                                                                                                   NAME/KEY: allele
LOCATION: 20259
                                                                                                                                          NAME/KEY: allele
LOCATION: 14968
OTHER INFORMATION:
                                                                                                                                                                                 OTHER INFORMATION: 99-16074-266 : polymorphic
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-C
                   OTHER INFORMATION:
                            NAME/KEY: primer_bind
LOCATION: 3547..3565
                                                                      NAME/KEY: primer_bind LOCATION: 3045..3062
                                                                                                  OTHER INFORMATION: 99-16066-123 :
                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 9871
                                                                                                                                                                                                                             OTHER INFORMATION: 99-16073-282 :
                                                                                                                                                                                                                                                                 LOCATION: 3262
OTHER INFORMATION: 99-16063-218 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 16158..16329
                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: 6231
                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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hes 168;
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primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COHEN, Daniel
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             99-16063.rp complement
                                                                                                                                      99-13817-215 : polymorphic base
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                                                                                                polymorphic base
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NAME/KEY: primer_bind
LOCATION: 20260..2027
OTHER INFORMATION: 99
            NAME/KEY: misc_feature
LOCATION: 285,982,2264,2273,2823,11227,11232,13663,13681,13842..13843
                                                                                                                     OTHER INFORMATION: 99-16066-123.mis
                                                                                                                                          NAME/KEY: primer_bind LOCATION: 20240..20258
                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                        NAME/KEY: primer_bind LOCATION: 14969..14987
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LOCATION:
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LOCATION: 6232..6250
OTHER INFORMATION: 99-16073-282.mis complement
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NAME/KEY: primer_bind
LOCATION: 9872..9890
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LOCATION: 3243..3261
OTHER INFORMATION: 99-16063-218.mis
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LOCATION: 14945.14991
OTHER INFORMATION: 99-13817-215.probe
NAME/KEY: misc_binding
LOCATION: 20236.20282
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LOCATION: 9848..9894
OTHER INFORMATION: 99-16074-266.probe
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LOCATION: 6208..6254
OTHER INFORMATION: 99-16073-282.probe
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LOCATION: 20137..2015
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LOCATION: 10119 .10136
OTHER INFORMATION: 99-16074.pu complement
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LOCATION: 20569..20588
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OTHER INFORMATION: 99-16073.rp
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LOCATION: 14754..14774
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                                                         99-16066-123.mis complement
                                                                                                                                                                               99-13817-215.mis complement
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GENERAL INFORMATION:

APPLICANT: Augustus, Meena
ITITLE OF INVENTION: Cancer Gene Determination and
ITITLE OF INVENTION: Sets
FILE REFERENCE: 689290-70
CURRENT APPLICATION NUMBER: US/09/969,708
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR APPLICATION NUMBER: US/60/237,425
         RESULT 7
US-09-944-456-2116/c
Sequence 2116, Application
Patent No. US20020115057A1
GENERAL INFORMATION:
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Best Local Similarity 84.4%;
Matches 168; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.7%;
Best Local Similarity 84.4%;
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                               18342 CTATTTAAAATACAAAAATTAGCCGGGTGTGGTGGCGGATGCCTGTAATCCCAGCTACTT 18283
                                                                                                                                     18162 AAAAAAAAAAAAAAAAAA 18144
                                                                                                                                                                                                                                                                           18282 GGGAGGCTGAGGCAGGAGAATCACTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCCAAGA
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                                                                                                                                                                                                                                                                                              2056 GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTTGGAGGTTGCAGTGAGGCTTGAGA 2115
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pred. No. 9e-21;
0; Mismatches 31;
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Pred. No. 6.2e-21;
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US-09-764-860-802
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PRIOR FILING DATE: 2000-09-18
PRIOR PRILING DATE: 2000-09-18
PRIOR PELLING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR PRILING DATE: 2000-09-25
PRIOR PRILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 802
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                                                                                                                                                                                                                                                                                                     Sequence 802, Application US/09764860 Patent No. US20020094953A1
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Best Local Similarity
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                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/764,860 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC008
                                                                                                                           Prior application data removed NUMBER OF SEQ ID NOS: 1198
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CURRENT FILING DATE: 2001-09-18
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             TYPE: DNA
ORGANISM: Homo sapiens
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                                                             LENGTH: 32248
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E OF INVENTION: Sets
REFERENCE: 689290-76
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RESULT 10
US-09-764-855-331
; Sequence 331, Application US/09764855
; Patent No. US20020119919A1
; GENERAL INFORMATION:
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                             APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA110
CURRENT APPLICATION NUMBER: US/09/764,855
CURRENT FILING DATE: 2001-01-17
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Matches
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Patent No. US20020119919A1
GENERAL INFORMATION:
Prior application data removed - consult PALM NUMBER OF SEQ \stackrel{\bullet}{\text{LD}} NOS: 334
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 334
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA110
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Pred. No. 1.4e-20;
0; Mismatches 33;
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US-09-764-853-878
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; ORGANISM: Homo sapiens
US-09-764-855-331
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PJZ06
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 878
                                                                                                                                                                                                                          Matches 167;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                          TYPE: DNA
5731 AAAAAAAAGAAAAAGAAAAA
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                                                                                                                                                                                                                                       Local Similarity
                            AAAAAACCACATAACATAAA 2195
                                                                TTGCGCCACTGCACTCCAGTCTGGGTCGGCAAGAGTGAGACTCCGTCTCAAAAACAAAACA 2175
                                                GGGAGGCTAAGGCAGGAGTCGCTTGAACCCAGGAGGTGGAAGTTGTAGTGGGCCAAGA
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Pred. No. 1.5e-20;
""@matches 33;
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Pred. No. 1.4e-20;
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US-09-946-807-1/c

Sequence 1, Application US/09946807 Patent No. US20020165144A1 GENERAL INFORMATION:

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                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/515,716 PRIOR FILING DATE: 2000-02-28
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                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: n-a
                                                                                                                                                                                                                                                                        OTHER INFORMATION: v=a
                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: (1)...(1531)
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OTHER INFORMATION: h=a
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LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
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OTHER INFORMATION: k-g
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LOCATION: (1)...(1531)
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Similarity
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Steinthorsdottir, Valgerdur
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US-09-795-668-1/c
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APPLICANT: Steinthorsdottir,
APPLICANT: Steinthorsdottir,
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
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      Matches 164;
                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
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LOCATION: (1)...(1531)
OTHER INFORMATION: h=a
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LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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                                                                                                                         NAME/KEY: misc_feature LOCATION: (1)...(1531)
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OTHER INFORMATION: d=a or
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LOCATION: (1)...(1531)
OTHER INFORMATION: b=g
NAME/KEY: misc_feature
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OTHER INFORMATION: w=a
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LOCATION: (1)...(1531)
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Score 146.6; DB 10;
Pred. No. 5.1e-20;
""" ematches 29;
                                           DB 10;
      Indels
                                       Length 1503841;
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US-09-795-686-1
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Query Match
Best Local Similarity
                                                                 NAME/KEY misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h-a or or
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v-a or gor
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: n-a or gor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
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OTHER INFORMATION: s-g or c
NAME/KEY: misc_feature
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OTHER INFORMATION: b=g
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OTHER INFORMATION: w=a or t/u
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LOCATION: (1)...(1531)
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OTHER INFORMATION: k-g or t/u
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LOCATION: (1)...(1531)
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NAME/KEY: misc_feature
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OTHER INFORMATION: r-g
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LOCATION: (1)...(1531)
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                                                                                                                                                                                                                        Matches
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Patent No. US20020142416A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BEASLEY, Ellen et al.

TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PRITIE OF INVENTION: THEREOF FILE REFERENCE: CLOOL192
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39779 AAAAAAAAAAAAAAA 39794
                                                                                                     39659 AGGAGGCTGAGGCTGGAGAATTGCTTGAGCCCCATGAGGTGGACGTTGCAGTGTGCTGAGA
                                                                                                                                                          39599 CTACTAAAAATACAAAATTAGCTGGGTGTGGTAGTGGGTGCCTGTAATCCCAGCTACTC 39658
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/818,512 CURRENT FILING DATE: 2001-03-28
                                                         39719
                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(116592)
OTHER INFORMATION: n = A,T,C or
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                        2176 AAAAAACCACATAACA 2191
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                                                                                                                                                                                                                                    Local
                                               TTGCGCCACTGCACTCCAGTCTGGTCGGCAAGAGTGAGACTCCGTCTCAAAAACAAAACA 2175
                                                                                                                             GGGAGCCTGAGGCATGAGAATCACTTGAACTCGGGAGGTGGAGGTTGCAGTGAGCTGAGA 2115
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Similarity 84.2%;
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                                                                                                                                                                                                              Score 146.4; DB 10; Length Pred. No. 3.4e-20; 0; Mismatches 31; Indels
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Search completed: February 14, 2003, 19:51:07 Job time: 2394.54 secs

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Title:
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                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
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                                                                                                                                    US-09-509-595B-2
2902
1 MATDAALRRLLRLHRTEIAV......DGILQWAIQSMARPAAPFPS 545
                                       283224 seqs, 96134422 residues
                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                      March 13, 2003, 17:51:42; Search time 21 Seconds (without alignments) 2494.917 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
      283224
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	U	4	· w	N	-	NO.	Result	•
151.5	151.5	152	152	152	152	152.5	152.5	153	154	155	157.5	159	160	161	168	168.5	171	178.5	179.5	186.5	194.5	194.5	206	217	219	219.5	221.5	273.5	Score		
5.2	٠	٠	•	5.2	•		•	•	•	5.3				5.5		٠		6.2	٠	6.4	6.7	6.7	7.1	7.5	7.5	7.6	7.6	9.4	Match I	Query	de
1479	728	1736	1204	1049	810	839	813	1006	1146	839	1201	958	350	684	1237	660	825	3942	404	607	5262	4957	1787	1051	371	1829	3938	530	Length I		
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5			hypothetical prote	collagen alpha líi	small GTP binding		Ca	1 relate	H		hypothetical prote	7		hypothetical prote	3	BHLF1 protein - hu	hypothetical prote	G)	ĸ	othetical p	protein -		ď	TIF1 protein - mou	phosphoprotein 75	hypothetical prote	soon protein -	Mi-2 autoantigen 2	ription		

44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
144 144	144.5	146	147	147	148	148.5	148.5	149	149	149.5	149.5	150	150.5	151.5
5.0	5.0	5.0	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.2	5.2	5.2	5.2	5.2
649	1214	574	1093	574	640	1400	283	2187	1207	1320	1151	2274	801	1532
N	N	N	Ν	N	N	N	N	ν	ν	N	N	N	N	N
A87913 T46500	JC2069	T38819	I38533	T43556	T08179	T31555	T11644	T30826	T00378	JC5630	T18535	T30258	T29018	A61262
protein B0205.10 ( hypothetical prote	zinc-finger protei	wiskott-aldrich sy	AF17 protein - hum	Wiskott-Aldrich sy	LRG5 protein - Chl	hypothetical prote	hypothetical prote	nascent polypeptid	KIAA0641 protein -	TCOF1 protein - mo	high molecular mas	adenomatous polypo	hypothetical prote	collagen alpha 1(X

## ALIGNMENTS

PRESILT 1  1855[8]  Mi - 2 autcontigen 240 kBe protein - human (fragment) C; Species; Homo sapiens (man) C; Chate: 06:5ep;1996 #sequence_revision 06:5ep:1996 #text_change 05:Nov-1999 C; Coccession: 13658; Milasena, D, S; O'Brian, C.A.; Frank, M.B.; Targoff, I.N. A; Title: Molecular analysis of analysis of santigenic region of the 240-kD protein of Milasena, D, S; O'Brian, C.A.; Frank, M.B.; Targoff, I.N. A; Title: Molecular analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.A.; Frank, M.B.; Targoff, I.N. A; Title: Molecular analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. A; Title: Molecular analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. A; Title: Molecular analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. A; Title: Molecular analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. A; Title: Molecular analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. A; Title: Molecular analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. A; Title: Molecular analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. A; Title: Molecular analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. B; Color analysis of analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. B; Color analysis of analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. B; Color analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. B; Color analysis of analysis of santigenic region of the 240-kD protein of Milasena; D; O'Brian, C.C. B; Color analysis of ana										
in of 15;	520 428	470 371	410 DSSALHPLLCVGPEGQQNLAPGAR	350 309	290 249	231 196	171 160	116 116	9.4%; Score 273.5; DB 2; 23.6%; Pred. No. 7.1e-09; vative 43; Mismatches 160;	RESULT 1 138558  Mi-2 autoantigen 240 kDa protein - human (fragment) C;Species: HOmo sapiens (man) C;Species: HOmo sapiens (man) C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_C;Accession: I38558 R;Ge, 0; Nilasena, D.S.; O'Brien, C.A.; Frank, M.B.; Targ J. Clin. Invest. 96, 1730-1737, 1995 A;Title: Molecular analysis of a major antigenic region of A;Reference number: I38558; MUID:96013633; PMID:7560064 A;Accession: I38558 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-530 <res> A;Cross-references: EMBL:U08379; NID:g761717; PIDN:AAC5022</res>
<b>▶→•</b>		PAKDDTASHEPALHRDDLESL 519 		DTTLVYKHLPAPPSAAPLPGL 409   :  DDHMEY334	EIDSGTWRCSSCLQATVQEVQ 349           :    RAPEGKWSCPHCEKBGVQWEA 308		LIQQVFESGGSKKCIQVGGEF 230	GTASPGSQLKAKPPKKPESSA 170    : ::   :  : GPGHKRRSKSPRVPD 159	; Length 530; ; Indels 127; Gaps	t) 6 #text_change 05-Nov-1999 1.B.; Targoff, I.N. region of the 240-kD protein of Mi-2 560064 BJ

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hypothetical protein F26F12.7 - Caenorhabditis elegans c;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te: C;Accession: T34239 R;Wilson, R.; Bentley, D.; Gattung, S.
R;Wilson, R.; Bentley, D.; Gattung, submitted to the EMBL Data Library, A;Description, The sequence of C. el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Dieck, S.; Sanmarti-Vila, L.; Languacse, A., A., A., A., A., Cell Biol. 142, 499-509, 1998
A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A;Reference number: 222249; MUID:98345363; PMID:9679147
A;Accession: T42761
A;Accession: T42761
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3938 <DIE>
A;Residues: 1-3938 <DIE>
A;Residues: 1-3938 <DIE>
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C; Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bassoon protein - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Description: may be involved in cytomatrix organization at ;Note: component of the presynaptic cytoskeleton ;Keywords: coiled coil; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 VDLSQPRKGRKPPAVPKALVPPPRLPTKRKAS--EEARAAAPAAL-----TPRGTAS 153
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                                                                                                                                                                                                                                                    L-----HRDDLESLLSEHTFDGILQWAIQSM-----ARPAAPFPS 545
                                                                                                                                                                                                               LSDTGYSSDGVSSSQSEIT--GVVQQEVEQLDSAGVTGPRPPSPS
                                                                                                                                                                                                                                                                                        V------PPGTPKAKSGVKRTDPATPVVKPVP-EAPKSGEAEEPVPKPYSQDLSRSPQS
                                                                                                                                                                                                                                                                                                              AFHWRCHFPAGTSRPGTGL-RCRSCSGDVTPAPVEGVLAPSPARLAPGPAKDDTASHEPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGE---EVRGP--PGEPLAGMDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TMPKERAACPLCQAELNVGSRGPANYNTCTACKLRVCTLCGFNPTPHLVEKTEWLCLNCQ 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRPPGSGPGPGPTPGAKTEPGPRTGPGSGPGALAKTGGTPSPKHGRADHQAASKAAAKPK 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAEQTQGGLTGKLFGLGASLLTQASTLMSVQPEADTQGQPSPSKGPPKIVFSDASKEAG
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23.4%; Pred. No. 6.1e
Live 57; Mismatches
  elegans
                    S.
April 1996
                                                                      29-Oct-1999 #text_change
  cosmid F26F12
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C; Keywords:
            A; Cross-references: GB:L22343; NID:g402147; PID:g402148
                                                                                           R;Kadereit, S.; Gewert, D.R.; Galabru, J.; Hovanessian, A. J. Biol. Chem. 268, 24432-24441, 1993
A;Title: Molecular cloning of two new interferon-induced, A;Reference number: A49515; MUID:94043285; PMID:7693701
                                                                                                                                                                                  phosphoprotein 75 - human
C:Species: Homo sapiens (man)
C:Date: 17-Nov-1995 #sequence_revision
                                                                                                                                                                                                                                            RESULT 4
B49515
                                 A; Molecule type: mRNA
A; Residues: 1-371 < KAD>
                                                                 A; Status: preliminary
                                                                                      A; Accession: B49515
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A; Accession: T34239
A; Status: preliminary; translated from A; Molecule type: DNA
A; Residues: 1-1829 <WIL>
A; Cross: references: EMBL: U55373; PIDN: A
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A;Map position: 5
A;Introns: 110/3; 441/3; 801/2; 1244/3; 1693/2; 1784/1
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phosphoprotein
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18.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 219.5; DB 2
Pred. No. 3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:AAC25894.1; GSPDB:GN00023; CESP:F26F12.7 istol N2; clone F26F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PDSDQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----QKQARGSKTPAVSTPVIPPRSAPTKTRSAR 184
                                                                                                                                                                                17-Nov-1995 #text_change 10-Sep-1997
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Query Match 7.5%; Best Local Similarity 25.1%; Matches 68; Conservative 3

37;

Score 219; DB 2; Pred. No. 7.6e-06; 7; Mismatches 110

Length 371; Indels

110;

56;

Gaps

9

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RESULT 6
T20160
hypothetical
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A; Residues: 1-1051 <LED>
A; Cross-references: GB:S78221; NID:g998814; PIDN:AAB34290.1; PID:g998815
A; Cross-references: GB:S78221; NID:g998814; PIDN:AAB34290.1; PID:g998815
C; Superfamily: unassigned bromodomain proteins; bromodomain homology
F; 48-136/Domain: RING finger homology <RRN>
F; 925-981/Domain: bromodomain homology <BRO1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;le Douarin, B.; Zechel, C.; Garnier, J.M.; Lutz, Y.; Tora, EMBO J. 14, 2020-2033, 1995
A;Title: The N-terminal part of TIF1, a putative mediator of A;Reference number: S55259; MUID:95262642; PMID:7744009
A;Accession: S55259
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C;Date: 27-Oct-1995 #sequence_revision
C;Accession: S55259
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                                                                                                                                                                                                                                      NYPRSILTSLLLNSSQSSASEETVLRSDAPDSTGDQPGLHQENSSNGKSE-WSDASQKSP
                                                                                                                                                                                                                                                                                                                                                                                    RPPSNRTVQ-----SPNSSVPSPGLAGPVTMTSVHPPIRSPSASSVGSRGSSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSPMIDLSAPVGGSYN------LPSLP-DIDCSSTIMLDNIARKDTGVDHA---QP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYGRLQPILDSFPKDVDLSQPRKGRKPPAVPKALVPPPRLP-----TKRKA 134
                                                                                                                                                                   VHVGETRKEDDPNEDWCAVCQNGGELLCCEKCPKVFHLTCHVPTLTNFPSGEWICTFCRD
                                                                                                                                                                                                     LALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQ
                                                                                                                                                                                                                                                                                                                                            SASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKK-----CIQVGGEFYTPSKFEDS
                                                                                                                                                                                                                                                                                                                                                                                                                   RLPTKRKASEEARAAAPAALTPR-GTASPGSQLKAKPP-KKPESSAEQQRLPLGNGIQTM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STAILDFWRVLFKDYNLERYGRLQPILDSFPKDVDLSQ----PRKGRKPPAVPKALVPPP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKSRSEEIIDG----TSEMNEGKRSQKTPSTPRRVTQGAASPGHGIQEKLQVVDKVTQRKD
                                                                                             LSKPEVDYDCDVP
                                                                                                                              ATVQEVQPRAEEP 355
                                                                                                                                                                                                                                                                                                           -SSSKPAGADSTHKVPVV--MLEPIRIKQ--ENSGPPENYDFPVVIVKQESDEESRPQNT
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   protein
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     T14G8.1
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     Caenorhabditis
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A;Residues: 1-1787 <WIL>
A;Cross-references: EMBL:267881; PIDN:CAA91798.1; GSPDB:GN00028; CESP:T14G8.1
A;Experimental source: clone C52G5
R;Matthews, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A; Reference number: Z19955 A; Accession: T24924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, November A; Reference number: \mathtt{Z19231}
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A;Map position: X
A;Introns: 112/3; 45
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A; Residues: 1-1787 <WI2>
A; Cross-references: EMBL: Z67884; PIDN: CAA91810.1; GSPDB: GN00028; CESP:T14G8.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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383
                                                                                                                      429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 EISAAI-----GLTDVDVDYEQEEFQSITNLKN-----FSSLVKPYILKVNPGTN 130
                                      GVLA------PSPARLAPG--PAKDDTASHEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQTMSASVQR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAILDFWRVLFKDYNLERYGRLQPILDSFPKDVDLSQPRKGRKPPAVPKALVPPPRLPT
KILSWRWKEISYPEPLECKEGEEASKDDVFLKPP
                                                                                                                  APGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAP---VE 485
                                                                                                                                                                                                  LRSAGEEVRGPPGEPL-AGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNL 428
                                                                                                                                                                                                                                            LCDTCTRAYHVACIDENMEQPPEGDWSC-----
                                                                                                                                                                                                                                                                                    CCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEPPVETPLPPG
                                                                                                                                                                                                                                                                                                                          RAAAKVDKRKAALESARASKRAR-KEQGVV-----EENHQEN---CEVCNQDGELM
                                                                                                                                                                                                                                                                                                                                                                                                                                               AVAMSSGDVPGARGAVEGILIQQVFESGGSKKCIQVGGEFYTPSKFEDSG-SGKNKARSS
                                                                              ----YCRICKETSNILLCDTCPSSYHAYCIDPPLTEIPEGEWSCPRC---IIPEPAQRIE
                                                                                                                                                                                                                                                                                                                                                              SGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVCRDGGELI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKII---
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                                                                                                                                                              -EPAKANMD-
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C; Species: Homo sapiens (man) C; Date: 24-Mar-1999 #sequence C; Accession: T03455

#sequence\_revision

24-Mar-1999 #text\_change 21-Jul-2000

RESULT T03455

ALR protein - human

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ALR protein - human ("Species: Homo sapiens (man) ("Species: Homo sapiens (man) ("C. Species: Homo sapiens (man) ("C. Species: To. 1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000 ("C. Accession: T0.3454 ("R. Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapal: Oncogene 15, 549-560, 1997 ("C. Prasad, R.; Structure and expression pattern of human ALR, a novel gene with starked the complex of the complex control of the complex control of the control 
                A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule
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C:Superfamily: human ALR protein
C:Keywords: alternative splicing
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A.Title: Structure and expression pattern of human ALR, a novel gene with stron A; Reference number: Z14954; MUID:97388474; PMID:9247308
A; Accession: T03455
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A; Residues: 1-4957 < PRA>
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19.9%; Pred. No. 0.002.;
19.9%; Mismatches 173;
                                                                              ession pattern of human ALR, a novel gene with strong MUID:97388474; PMID:9247308
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                                                                                                                                                               Druck, T.; Rallapalli,
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C; Genetics:
A; Gene: SPA
A; Map position:
                                                   A;Cross-references: EME
A;Experimental source:
                                                                                        A; Molecule type: DNA
A; Residues: 1-607 <GE2>
                                                                                                                                                                                                             hypothetical protein SPAC2F7.07c - fission yeast (Schizosaccharomyces pombe) C:Species: Schizosaccharomyces pombe C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000 C:Accession: T38555; S58151
                                                                                                                       A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; submitted to the EMBL Data Library, July 1995
                                                                                                                                                   A; Reference number: Z21799
A; Accession: T38555
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C; Superfamily: human ALR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835 PALDDFSGLGEDTAPLDGIDAPGSQPEPGQTPGSLASELKGSPVL----LDPEELAPVTP 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AALTP--RGTASPGSQLKAKPPKKPESSAEQQRLPLGNGTQTMSAS--VQRAVAMSSGDV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 PILDSF-----PKD-VDL--SQPRKGRKPPAVPKALVPPPRLPTKRKASEEARAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                            APSPARLAPGPAKDDTASHEPALHRDDLESLLSEHTFDGILQWAIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LIQCRHCERWMHAGCESLFTEDDVDH-----APDEGFDCVSCQ----PYVVKPVA 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGTDVLRCTHCAAAFHWRC-----HFPAGTSRPGTGLRCRSCSGDVTPAPVEGVL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLDPPLLTVPKGGWKCKWCVSCMQCGAAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACSQCSQCYHPYCVNSKITKVMLLKGWRCVECIVCEVCGQASDPSRLLLCDDCDISYHTY 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTAISGGKAEGEKGRRRSSPARSRIKQGRSSSFPGRRRPRGGAHGGRGRGRARLKSTASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEVYPECKQTAGRGS------PCEEQEEPRAPVAPTPPTLIKSDIVNEISNLSQGDA 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAPLA---LPSDPQLHQKNED------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSG-----KNKARSSSGPKPLVRAKGA-----QGAAPGG---GEARLGQQGSV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                             EMBL:Z50142; NID:g1052783; PIDN:CAA90494.1; PID:g1052790; ce: strain 972h-; cosmid c2F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <PRA>: EMBL:AF010403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SYTHCGPCASLVTCP-----ICHAPYVEEDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.7%; Score 194.5; DB 2; 19.9%; Pred. No. 0.0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ECAVCR-----DGGELICCDGCPRAFHLA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NID: g2358284; PIDN: AAC51734.1; PID: g2358285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                Rajandream,
                                                                                                                                                                                                                                                                                                                                                                          FEGV -- WLTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                  Walsh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                              GSPDB:G
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C:Species: Schizosaccharomyces pombe C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000 C;Accession: T37778; S62475 R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, October 1995 A;Reference number: Z21745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z54366; NID:g1019812; PIDN:CAA91193.1; PID:g1019817; GSPDB:GN00A;Experimental source: strain 972h-; cosmid c16C9
C;Genetics:
A;Gene: SPAC16C9.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-404 <BA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: T37778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHD finger protein - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                            508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
                                                                                                                                                                                                                                                                                                                                                                                                                  294 KNEDECAVCRDGGELICCDGCPRAFHLACLSPPL--REIPSGTWRCSSCLQATVQEVQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 TASPGSQLKAKPPKKPESSAEQQRLPLGNGIQTMSASVQRAVAMSSGDVPGARGAVEGIL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                 -EPALHRDDLESLLSEHTFDGIL
                                                                               CDTFYHKNCKEHA-----KKCSHD--SIGKKGMRVPKNAVVIRTPLVLDTTSNT
                                                                                                                         CAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAPVEGVLAPSPARLAPGPAKDDTASH- 507
                                                                                                                                                                                                                                                                                                                                AEEPRPQEP - - - - -
                                                                                                                                                                                                                                                                                                                                                                     RNVDYCSACGGRGLFICCEGCPCSFHLSCLEPPLTPENIPEGSWFCVTC---SIKSHHP-
                                                                                                                                                                                     -- DEFSALPTGSSITNL-
                                                                                                                                                                                                                          VYKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTD----VLRCTH
                                                                                                                                                                                                                                                                         ----PKHPLSIWSQLYDWIDSQNPSQYRLPDDLVHYFHGISRGDTGAYKETEGEMDT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDHVTP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGPEGQQNLAPGARCGVCG-DGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLR---CRSC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRNVTVYSNQK---HLGNE---SENFNDM----EGRAEDISSNELL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGDVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SISSFFRGVGSGVMGEYIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GL----PSAAPLPGLDSSALHPLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -IPSGTWRCSSCLQATV-----QEVQPRAEEPR------PQEPPVETPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARLGQQGSVPAPLALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQQVFESGGSKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAKDLSDISSSSMKKANNSSK----PLFSGKLTFKANI-----PVPTSEVVTENNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLPDDAWYCNECKHHSLYNELDEQEELESNVKEEGTMVDVWMQLCTYIDSHNPIQFHLPH 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PTPEEYP----YRYNNDYCSACHGPGNFLCCETCPNSFHFTCIDPPIEEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCHKSALVSQSILACDYCNSYWHPDCLNPPLATLP-SNLRKWKCPNH 456
                                                                                                                                                                                                                                                                                                                      ---PVETPLPPGLRSAGEEV-RGPPG---EPLAGMDTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 179.5; DB 2;
Pred. No. 0.0017;
Prematches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.001;
4; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TDVLKHLKSSRRSNGEERDPLL-LKSKSGTPILC
                                                                                                                                                                             -AYCGYCSKPSMGACWVYGCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75;
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                                                                                                                                                                             259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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hypothetical protein At2g37520 [imported] - Arabidopsis thaliana N; Alternate names: hypothetical protein F13M22.2
                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                           δÃ
                                                         T02518
                                                                             RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: may be involved in cytomatrix organization at the site of neurotransmi A;Note: component of the presynaptic cytoskeleton C;Keywords: coiled coil; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-3942 <DIE>
A;Residues: 1-3942 <DIE>
A;Cross-references: EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810
A:Fxnerimental source: strain 129 SVJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bassoon protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Ju1-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 9F1
A; Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, J. Cell Biol. 142, 499-509, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T42730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: bassoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat Reference number: Z22249; MUID:98345363; PMID:9679147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: T42730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                  685
                                                                                                                                                                                     503 DTASHEPAL----HRDDLESLLSEHTFDGILQWAIQSM-----ARPAAPFPS 545
                                                                                                                                                                                                                                                                                                                                                                                                                                 525 GEPAP-LPLPTPQQPPAGVP----HRAAGAAPLKQKGPQGLGQPSGSLPAKASPQATKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 QEVQPRAEEPRPQEPPVETPLPPGLRSAGE---EVRGPPG------EPLAGMDT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 PLCQAELNVGSRGPANYNTCTACKLQVCNLCGFNPTPHLVEKTEWLCLNCQTKRLLEGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405 GPTPGAKTEPGARTGPGSGPGALAKTGGTASPKHGRAEHQAASKAAAKPKTMPKERAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 TGKLFGLGASLLTQASTLMSVQPEADTQGQPSPSKGPPKIVFSDASKEAGPRPPGSGPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 PQPPLSTKPSTAEPRPPAG-----EAQGKSATTVPSGLGAGEQT-----QEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 PAKOPLGKPEQERSPRG-PGATQSGPR-----QAEAARATSVPGPT-QATAPPEVGRVS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 PKDVDLSQPRKGRKPPAVPKALVPPPRLPTKRKASEEARAAAPAALTPRGTASPG-SQLK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 AVC-----RDGGELICCDGCP-RAFHLACLSPPLREIPSGTWRCSSC-----LQATV 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 KPLVRAKGAQGA--APGGGEARLGQQGSVPAP-----LALPSDPQLHQKNEDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 AKPPKKPESSAEQQRLPLGNGIQTMSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 LNPKVMISGWQFLMGEFPSDELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                           DLSRSPQSLSDTGYSSDGVSSSQSEIT--GVVQQEVEQLDSAGVTGPRPPSPS
                                                                                                                                                                                                                                                                                   AAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAPVEGVLAPSP-----ARLAPGPAKD 502
                                                                                                                                                                                                                                                                                                                                     PQATKASPQATKASPQTTKASPQAKPLRATEPSKTSSSAQEKKTATPAKAEPVPKPP---
                                                                                                                                                                                                                                                                                                                                                                                  TLVYKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                         -PETTVPPGTP---KAKSGVKRTDPATPVVKPVPEAPKGGEAEEPVPKPYSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 178.5; D
Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3851/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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3942;

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24;

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524

464

404 252 344 219

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A; Residues: 1-60 <BAN>
R; Baer, R.; Bankler, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A; Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A; Reference number: A03794; MUID:84270667; PMID:6087149
A; Contents: annotation; protein coding region
C; Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52
C; Superfamily: human, herpesvirus 4 BHLF1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus A;Reference number: A93065; MUID:85035713; PMID:8092825
A;Accession: A03742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BHLF1 protein - human herpesvirus 4 (strain B95-8)
C:Species: human herpesvirus 4, Epstein-Barr virus
C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 23-Aug-1997
C:Accession: A03742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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A;Gene: F13M22.2; At2g37520
A;Gene: F13M22.2; At2g37520
A;Map position: 2
A;Introns: 189/3; 212/3; 282/3; 304/1; 366/2; 388/2; 415/3; 433/2; C;Superfamily: Arabidopsis thaliana hypothetical protein F4P12.380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Experimental source: cultivar Columbia
R:Lin, X:; Kaul, S:; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02518; G84793
R;Rounsley, S,D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.
A;Reference number: Z14677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE002093; NID:g3236235; PIDN:AAC23623.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-825 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: G84793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AC004684; NID:g3236234; PID:g3236235
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A;Residues: 1-825 <ROU>
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                                                                                                                                                                                                                                                                                             ;Superfamily: human herpesvirus 4 BHLF1 protein
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Best Local Similarity
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Best Local
                       157
                                                                                172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 PRPQEPPVETPLPPGLRSAGEEVRG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 NEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEE 354
QLKAKP----PKKPESSAEQQRLPLGNGTQTMSASVQRAVAMSSGDVPGAR------
                                                                                                                PRKGRKP-----PAVPKALVPPPRLPTKRKASEEARAAAPAALTPR-----GTASPGS 156
                                                        PGAGQRPSGPTGGRPAAPGA----PGTPA--APGPGGGAAVPSGATPHPERGSGPADPPA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDDMCSICGDGGDLLLCAGCPQAFHTACLK--FQSMPEGTWYCSSCNDGPISSKKATTTD 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.9%; Score 171; DB 2; Length 825; 34.1%; Pred. No. 0.011;
                                                                                                                                                                                                            5.8%; Score 168.5; DE 23.4%; Pred. No. 0.012;
                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                         Pred. No. 0.016; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                               192;
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                                                                                                                                                                               Indels
                                                                                                                                                                                                                                    Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                               175;
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                                                                                                                                                                         Gaps
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PT RE REL RESERVE RESE

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1043 TPGGRTLERDVGCTRHQSVQTE-----DG-----TGGMARAVAKAALS-PVQEHETG--R 337 CSSCLQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGEEVRGP---PGEPLA--GMD---

389 1089 VPAPLALPSDP--QLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWR 336 LG---APRQVAVRRLGRQESPLSLGADPLL-PEGASRPPVSSKEKESPGGAEACTPPRAT 1042 930 RVQSAEKLG----ASLSADKKGALRKHSLEVGHPDFRKDFHGELALHSLAESDGETPPVEG 170 AEQQRLPLGNGIQTMSASVQRAVAMSSGDV--PGARGAVEG-ILIQQVFESGGSKKCIQV

GGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGA-----QGAAPGGGEARLGQQGS

278

986

116 PAVPKALVP-----PPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESS 870 PLSPLAHTPSPTQASPPPLPGHTVGSSHTTQSFPAKLHSSPPVVRPRPKSAEPPRSPLLK 929

169

Query M Best Lo Matches	C; Genetics: A; Map posit A; Note: Int	A; Molecule 1 A; Residues: A; Cross-refe A; Experiment	A; Accession A; Status:	submit A;Des	C; Date: 21-J; C; Accession:	protein C; Speci	RESULT	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	DЪ	Qy	Db
Query Match Best Local Matches 11	etics posi e: In	cule dues s-re	essic	ript	essic	in ki	r 14	584	492	524	443	464	416	417	356	376	317	316	261	286	204	226
<pre>Watch 5.8%; Score 168; DB 2; Length 1237; Local Similarity 26.4%; Pred. No. 0.025; res 111; Conservative 41; Mismatches 180; Indels 88; Gaps 22;</pre>	ion: 19p13.2	type: DNA 1-1237 <lam> erences: EMBL:AD000092; al source: cell line 5</lam>	A;Notestance number: 222906 A;Notestance number: 422906 A;Status: preliminary: translated from GB/EMBL/DDBJ	submitted to the EMBL Data Library. November 1996 A; Description: Characterization by genomic sequence analysis of a gene-rich 111 kb	_revision 21-Jan-2000 #text_change 21-	<pre>protein kinase homolog R31240_1 (imported) - human (fragment) C; Species: Homo saplens (man)</pre>		GATPHPERGSGPADPPAAARLPPERQEPRLPQD 616	PARLAPGPAKDDTASHEPALHRD 514		VLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAPVEGVLAPS 491	PERGSGPADPPAAARLPPERQEPRLPQDLAAAQRCPAGPPPTRSGAAAQRTHRRPPGCPR 523	PLLCVGPEGQQNLAPGARCGVCGDGTD 442	RGHPPPGAGQRPSGPTGGRPAAPGAPGTPAAPGPGGGAAVPSGATPH 463	RPQEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALH 415	G9PTTRSGAAAQRTHRRPPGCPRSARNPGCPRTWRRRSGAQ416	AFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEP 355	APGTPAAPGPGGGAAVPSGATPHPERGSGPADPPAAARLPPERQEPRLPQDLAAAQRCPA 375	AQGAAPGGGEARLGQQGSVPAPLAI	RRSGAQRGAAPG 315		

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Search completed: March 13, 2003, 17:54:29 Job time: 30 secs
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N;Alternate names: hypothetical protein YM9916.14
C:Species: Saccharomyces cerevisiae
C:Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C:Accession: S52835
R;Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, April 1995
A;Reference number: S52814
A;Accession: S52835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1149 LEVVEERTTLSGPRSKPASPKLSPEP--QTPSLAPAKCSAPSSAVTPVPPA--SLLGSGT 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1205 ----
                                                                         426 GSWSHPENSRLIMTCDYCQTPWHLDCVPRASFKNLGSKWKC
                                                                                                                                                                                       384 --PLAG--MDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGD 439
                                                                                                                                                                                                                               318 TLKKIESNFIKQNNNYKIFAKLLFNIDSHNPKQFQLPNYIKETFPAVKTGSRGQYSDEND 377
                                                                                                                      440
                                                                                                                                                      378 KIPLTDRQLFNTSYGQSITKLDSYNPDTHIDSNSGKFLICY----
                                                                                                                                                                                                                                                                      258 ENEDFCSACNQSGSFLCCDTCPKSFHFLCLDPPIDPNNLPKGDWHCNECKFKIFINNSMA 317
                                                                                                                                                                                                                                                                                                                                                    294 KNEDECAYCRDGGELICCDGCPRAFHLACLSPPL--REIPSGTWRCSSC-----LQA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 DVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAPV--EGVLAPSPARLAPGP 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 -----TTLV-YKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGT 441
                                                                                                              GT-----DVLRCTHCAAAFHWRCHFPAGTSRPGTGLRC 472
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                                                                                                                                                                                                                                                                                                                                                                                         85; Indels 54; Gaps
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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                   NO.
             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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016102 drosophila	016102	υı	887	•	181	-
droso	8FAS80	U	627		181	
homo sapier	Q916V0	4	5147	٠	182	
zea	Q945C8	10	810		182.5	_
	Q8VEC8	11	556		182.5	_
9 arab	048579	10	2228		184	~
5 homo	Q9UPAS	4	3926		184.5	_
	043161	4	3851	6.4	184.5	٠.
o	Q8T0U1	S	878	6.4	184.5	٠.
	Q96QT6	4	704	6.4	186	_
Q9vdk5 drosophila	Q9VDK5	υı	1139	6.4	186.5	~
drosophi	Q9W410	σ	898	6.5	187.5	
6 ratt	Q9JKS6	11	5085	6.5	188	-
homo	Q96BD5	4	680	6.6	192	_
homo	014686	4	5262	6.7	194.5	•
	014687	4	4957	6.7	194.5	w
mus mu	Q9QYX7	11	5038	6.8	9	_
oryz	Q9LGS5	10	607	6.8	197.5	
_	Q96T95	4	885	7.2	209	٠.
homo	Q9Н930	4	245	7.3	210.5	-
mus	Q924W6	11	1209	7.4	214	w
Bug	Q9D1Q8	11	429	7.4	214	
4 mus	Q8R154	11	516	7.5	217	_
homo	Q9BQQ4	4	1214	7.5	217.5	_
	Q14977	4	408	7.5	219	•
815 caenorhabdi	Q19815	υı	1829	7.6	219.5	w
O88778 rattus norv	088778	11	3938	7.6	221.5	7

## ALIGNMENTS

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RESULT 1
075745
                            Query Match
                                   Pfam; PF00628; PHD; 1.
Pfam; PF03142; SAND; 1.
Pfam; PF03172; Sp100; 1.
SMART; SM00249; PHD; 1.
SMART; SM00258; SAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      075745;
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                            SEQUENCE
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Paloti A., Peltonen L.,
Lehrach H., Yaspo M.L.;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98061087; PubMed=9398840;
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCBI_TaxID=9606;
                                                                                             InterPro; IPR000770; SAND_domain.
InterPro; IPR004865; Sp100.
InterPro; IPR001965; Znf_PHD.
                                                                                                                                     Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases EMBL; AJ009610; CAA08759.1; -.
                                                                                                                                                                       SEQUENCE FROM N.A.
Lee Y.S., Francis F.,
                                                                                                                                                                                                            "An autoimmune disease, APECED, caused by mutations in a novel gene featuring two PHD-type zinc finger domains."; Nat. Genet. 17:399-403(1997).
                                                                                                                                                              Yaspo M.L.;
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Last sequence update)
Last annotation updat
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  Score 2687;
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  DB 4;
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Length 515;
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RESULT 2
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ID Q920
AC Q920
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DT 01-M
DT 01-J
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GN AIRE
GN AIRE
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RP SEQU
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RT "Thee
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RN [2]
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STRAIN=129SV;

MEDLINE=99160890; PubMed=10049735;

Mittaz L., Rossier C., Heino M., Petersen P., Krohn K.J.E.

Morris M.A., Shimizu N., Antonarakis S.E., Scott H.S.;

"Isolation and characterization of the mouse Aire gene.";

"Isolation and characterization of the Mouse Aire gene.";
                                                                                                                                                                                                                Karin B., Schweiger M., Wertz K.,
Rosenthal A., Lehrach H., Yaspo M.
"The mouse Aire gene: comparative
organization and expression.";
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat.
AIRE protein (AUTOIMMUNE regulator).
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Query Match
Best Local S
Matches 395
                                                                                                                                                                                                                                             Interpro; IPRO00770; SAND_domain.
Interpro; IPRO04865; Sp100.
Interpro; IPRO04865; Sp100.
Interpro; IPRO01965; Znf_PHD.
Interpro; IPRO01841; Znf_ring.
Pfam; PF00628; PHD; 2.
Pfam; PF003172; Sp100; 1.
SMART; SM00001; EGF_like; 1.
SMART; SM000249; PHD; 2.
SMART; SM000249; RING; 2.
SMART; SM00258; SAND; 1.
SMART; SM00258; SAND; 1.
SEQUENCE 552 AA; 59042 MW; BF30
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-199) to the EMBL EMBL; AJ132243; CAB36909.1; --
EMBL; AJ007715; CAB07620.1; --
EMBL; AF079536; AAD20444.1; --
EMBL; AF128773; AAB66442.1; --
EMBL; AF128773; AAF36482.1; --
EMBL; AF128773; AAF36481.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-NOD, AND SJL;
Shi J.D., Wang C.Y., Marron M.P.,
Davoodi-Serniromi A., She J.X.;
"Complete genomic sequence, gene and the gene";
mouse Aire gene";
      243
                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halonen M.,
Ulmanen I.,
                            185
                                                184
                                                                      125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Autoimmunity 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Autoimmune Regulator Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       She J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Chromosomal Localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang C.Y., Shi J.D., Davoodi-Semiromi A., She J.X.;
"Cloning of Aire, the mouse homologue of the autoimmune regulator
(AIRE) gene responsible for autoimmune polyglandular syndrome type
(ASPI).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=B6; TISSUE=THYMUS; MEDLINE=99168902; PubMed=10049587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
SEQUENCE FROM N.A.
                                                                                                                  65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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KNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVC
                     MAASVQRAVTVASGDVPGTRGAVEGILIQQVFESGRSKKCIQVGGEFYTPNKFEDPSGNL
                                 MSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKKCIQVGGEFYTDSKFED-SGSG
                                                                            PPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQT
                                                                                                          LPPRPPTKRKALEEPRATPPATLASKSVSSPGSHLKTKPPKKPDGNLESQHLPLGNGIQT
                                                                                                                                                                                                                                                                                                                                                                                           MGI:1338803;
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                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                              IPR000561;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kolmer M.;
of the mouse AIRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pelto-Huikko M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Y.,
                                                                                                                                                                                                                                                                                                                                                                                          Aire
                                                                                                                                                                                                             69.1%;
71.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marron M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Aire)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                            Score 2005; DB 11;
Pred. No. 6.3e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete re).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palvimo J.,
                                                                                                                                                                                                                                            BF30F8F66B71239A CRC64;
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  structure
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Best Local
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                                                                                                                                                                                                                                                                                             Pfam; PF01342; SAND; 1.
Pfam; PF03172; SP100; 1.
SMART; SM00001; EGE_like; 1.
SMART; SM00249; PHD; 2.
SMART; SM00258; SAND; 1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruan Q.G., Wang C.Y., Shi J.D., She J.X., "Expression and alternative splicing of t gene (Aire).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9JLW9;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000561; EGF-like.
InterPro; IPR000770; SAND_domain.
InterPro; IPR004865; Sp100.
InterPro; IPR001965; Znf_PHD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1338803; Aire.
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                                                                                               P-VEGVLAP-SPARLAPGPAK--DDTASHEPALHRDDLESLLSEHTFDGILQWAIQSMAR
  SWILTQDSTAILDFWRVLFKDYNLERYGRLQPILDSFPKDVDLSQPRKGRKPPAVPKALV 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGRPGPAPSARCSVCGDGTEVLRCAHCAAAFHWRCHFPTAAARPGTNLRCKSCSADSTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00628; PHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ited (FEB-1999) to the EMBL/GenBank/DDBJ databases AF128116; AAF36461.1; ...
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                                                                                                                                                                                                        Conservative
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                          Score 1991; DB 11;
Pred. No. 5.5e-127;
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                                                                                                                                                                                                   7;
                                              RESULT
Q9JLXO
ID
Q9JLXO
Q9GLX
AC
Q9GLX

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Query Match
                                              SMART; SN
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                           MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-B6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9JLX0
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                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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Pfam; PF00628; PHD; 2.
Pfam; PF0132; SAND; 1.
Pfam; PF03172; Sp100; 1.
SMART; SM00001; EGF_like; 1
SMART; SM00249; PHD; 2.
SMART; SM00184; RING; 2.
SMART; SM00258; SAND; 1.
                                                                                                                                                                                                                                                                                                         "Expression and alternative gene (Aire).";
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9JLX0;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                       MGI:1338803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLAETPPFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HDGGELICCDGCPRAFHLACLSPPLQEIPSGLWRCSCCLQGRVQQNLSQPEVSRPPELPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAA---PFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-VEGYLAP-SPARLAPGPAK--DDTASHEPALHRDDLESLLSEHTFDGTLQWAIQSMAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGTPGEAVPTSGPRPAPGLAKVGDDSASHDPVLHRDDLESLLNEHSFDGILQWAIQSMSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETPILVGLRSASEKTRGPSRELKASSDAAVTYVNLLAPHPAAPL--LEPSALCPLLSAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPPRPPTKRKALEEPRATPPATLASKSVSSPGSHLKTKPPKKPDGNLESQHLPLGNGIQT
                                                                                                                                                                                                                                                                                    AF128115; AAF36460.1;
                                                                                                                                                                      IPR000770; $; IPR004865; $; IPR001965; ; IPR001841;
                                                                                                                                                                                                                                                                                                (FEB-1999) to the
                                                                                                                                                                                                                                        IPR000345; CytC_heme_bind
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O (TrEMBLrel. 15,
O (TrEMBLrel. 15,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                  Ā,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      545
                               CYTOCHROME_C; 58913 MW; 7
                                                                                                                                                                                                                                                                       Aire.
                                                                                                                                                                                       SAND_domain.
Sp100.
Znf_PHD.
                                                                                                                                                                     Znf_ring.
 68.6%;
                                                                                                                                                                                                                                                                                                                                .D., She J.X. splicing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
 Score 1989.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                               UNKNOWN_1.
77C75E773B48B72C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551
                                                                                                                                                                                                                                                                                                                     .;
the mouse autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
 DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                      databases
Length 551;
                                                                                                                                                                                                                                                                                                                                  regulator
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Best Loc Matches

4

Local

15;

Gaps

8

242

183

124

184

123

64 63

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InterPro; IPR000345; Cyrc_heme_bind.
InterPro; IPR000561; EGF-like.
InterPro; IPR000770; SAND_domain.
IpterPro; IPR004865; Sp100.
InterPro; IPR004865; Znf_PHD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00628; PHD; 2.
                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
[1]
                                                                                                                             Ruan Q.G., Wang C.Y., Shi J.D., She Texpression and alternative splicing gene (Aire).";
                                                                                             MGI:1338803;
                                                                                                                                                                                                                                                                                                                                                                                    PLAETPPFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                       P-VEGVLAP-SPARLAPGPAK--DDTASHEPALHRDDLESLLSEHTEDGILOWAIOSMAR
                                                                                                                                                                                                                                                                                                                                                                                                          PAA---PFPS
                                                                                                                                                                                                                                                                                                                                                                                                                           PGTPGEAVPTSGPRPAPGLAKVGDDSASHDPVLHRDDLESLLNEHSFDGILQWAIQSMSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF128117; AAF36462.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGRPGPAPSARCSVCGDGTEVLRCAHCAAAFHWRCHFPTAAARPGTNLRCKSCSADSTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGQONLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPDSAAPLPGLDSSALHPLLCVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETPILVGLRSASEKTRGPSRELKASSDAAVTYVNLLAPHPAAPL--LEPSALCPLLSAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNKARSGSSLKPVVRAKGAQVTIPGRDEQKVGQQCGVPPLPSLPSEPQVNQ-NEDECAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNKARSSSGFKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKKCIQVGGEFYTPSKFED-SGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPPRPPTKRKALEEPRATPPATLASKSVSSPGSHLKTKPPKKPDGNLESQHLPLGNGIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWLLTQDSTAILDEWRYLEKDYNLERYGRLQPILDSFPKDVDLSQPRKGRKPPAVPKALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWLLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFPKDVDLNQSRKGRKPLAGPKAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                   (FEB-1999)
                                                                                                                                                                                                                                                                regulator.
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                              N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          545
                                                                                            Aire.
                                                                                                                  to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.6%;
                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                       Last sequence update)
                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
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37; Mismatches
                                                                                                                                                                                                            Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                  J.X
                                                                                                                                       of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7e-127;
ches 108;
                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                      mouse
                                                                                                                                                                                                              Muridae;
                                                                                                                                                                                                                                                                       update)
                                                                                                              databases
                                                                                                                                      autoimmune
                                                                                                                                                                                                            Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                      regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482
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  RESULT
Q9JLW7
                                                                                                                                                                                                                                                                           Qy
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                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                   Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
STRAIN=B6;
Ruan Q.G., Wang 'Expression and gene (Aire).";
                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                              SEQUENCE FROM N.A.
                                                                                                                      AIRE.
                                                                                                                                          01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                Q9JLW7;
                                                                                                                                Autoimmune regulator
                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01342; SAND; 1.
Pfam; PF03172; Sp100; 1.
SMART; SM00001; EGF like; 1.
SMART; SM000249; PHD; 2.
SMART; SM00184; RING; 2.
SMART; SM00258; SAND; 1.
PROSTTE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAASVQRAVTVASGDVPGTRGAVEGILIQQVFESGRSKKCIQVGGEFYTPNKFEDPSGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWLLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFPKDVDLNQSRKGRKPLAGPKAAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   547 AA;
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         C.Y., Shi J
alternative
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71.5%;
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        splicing
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37; Mismatches 105;
                                                                             Craniata; Vertebrata; p
Sciurognathi; Muridae;
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Pred. No. 6.2
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                     J.X.
         of
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        the
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         mouse
                                                                                                                                          update)
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        autoimmune
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                                                                                         Euteleostomi;
                                                                              Murinae;
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477 482 417 422 359 362 299 302

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Q9JLW8;

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Autoimmune AIRE.

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> 125 184

124 65 64

RESULT
Q9JILM8
ID Q9
ID Q9
ID Q9
ID Q1
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SEQUENCE

FROM

EMBL; MGD; 1

regulator

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RESULT 7
Q9JLW5
ID Q9JL
AC Q9JL
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Best Local
             O9JLW5 PRELIMINARY;
O9JLW5;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00628; PHD; 2. Pfam; PF01342; SAND; 1. Pfam; PF03172; Sp100; 1. SMART; SM00001; EGF like; 1. SMART; SM00014; PHD; 2. SMART; SM00149; PHD; 2. SMART; SM00184; RING; 2. SMART; SM00258; SAND; 1. SMART; SM00258; SAND; 1. SMART; PS00190; CYTOCHROME_C; UNKNOWN_1. PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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InterPro;
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InterPro;
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MGD; MGI:1338803;
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                                                                                       PLAETPPFSS
                                                                                                                   EGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPA
                                                                                                                                                                                                                  HDGGELICCDGCPRAFHLACLSPPLQEIPSGLWRCSCCLQGRVQQNLSQPEVSRPPELPA
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                                                                                                                                                                                                                                                                                  PPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQT
                                                                                                                                                                                                                                                                                                                                                 PAA---PFPS 545
                                                                                                                                                                                                  ETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCVGP
                                                                                                                                                                                                                                                  KNKARSGSSLKPVVRAKGAQVTIPGRDEQKVGQQCGVPPLPSLPSEPQVNQKNEDECAVC
                                                                                                                                                    ----APSARCSVCGDGTEVLRCAHCAAAFHWRCHFPTAAARPGTNLRCKSCSADSTPT
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      regulator.
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                                                PRELIMINARY;
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l; Mismatches 8
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                      sequence update)
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Query Match
Best Local Similarity
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Pfam; PF01342; SAND; 1.
Pfam; PF03172; Sp100; 1.
SMART; SM00001; EGF_like; 1
SMART; SM00240; PHD; 2.
SMART; SM00184; RING; 2.
SMART; SM00258; SAND; 1.
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MGD; MGI:1338803; Aire
InterPro; IPR000345; CytC_heme_bind
InterPro; IPR000345; EGF-like.
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"Expression and alternative splicing of the mouse autoimmune gene (Aire).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000561; EGF-like.
InterPro; IPR000770; SAND_domain.
InterPro; IPR004865; Sp100.
InterPro; IPR001965; Znf_PHD.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE 489 AA; 52585 MW; BA09175B96C9824A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004865; InterPro; IPR001965; InterPro; IPR001841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQT
PLAETPPFSS
                                        PAA - - - PFPS
                                                                              EGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPA 482
-----APSARCSVCGDGTEVLRCAHCAAAFHWRCHFPTAAARPGTNLRCKSCSADSTPT 419
                                                                                                                                                                                                                                                                                                                                                              RDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEPPV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKKCIQVGGEFYTPSKFED-SGSG
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                                                                                                                                                                                                                                                                                             ETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCVGP 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt MAASVQRAVTVASGDVPGTRGAVEGILIQQVFESGRSKKCIQVGGEFYTPNKFEDPSGNL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWLLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFPKDVDLNQSRKGRKPLAGPKAAV
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489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
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Q9JLW6 Q9JLW6; Q9JLW6; 01-OCT-2000 (TrEMBLrel. 1 01-OCT-2000 (TrEMBLrel. 1 01-JUN-2002 (TrEMBLrel. 2

15, 15, 21,

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EGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPA
                                                                                                                                 ETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCVGP
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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Pfam; PF01342; SAND; 1.
Pfam; PF03172; Sp100; 1.
SMART; SM00001; EGF_like; 1.
SMART; SM00249; PHD; 2.
SMART; SM00184; RING; 2.
SMART; SM00258; SAND; 1.
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"Expression and alternative splicing of the mouse autoimmune gene (Aire).";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF128121; AAF36466.1; -.
MGD; MGI:1338803; Aire.
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01-OCT-2000
01-OCT-2000
01-JUN-2002
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InterPro;
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Mammalia; Eutheria;
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       KNKARSGSSLKPVVRAKGAQGR----DEQKVGQQCGVPPLPSLPSEPQVNQ-NEDECAVC
                             KNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVC
                                                                                                         MSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKKCIQVGGEFYTPSKFED-SGSG
                                                                                                                                                                                   PPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQT
                                                                                 MAASVQRAVTVASGDVPGTRGAVEGILIQQVFESGRSKKCIQVGGEFYTPNKFEDPSGNL
                                                                                                                                                             LPPRPPTKRKALEEPRATPPATLASKSVSSPGSHLKTKPPKKPDGNLESQHLPLGNGIQT
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488 AA; 52457 MW; 628EDC8A86
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IPR004865; Sp100.
IPR001965; Znf_PHD.
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IPR000561; EGF-like.
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2 (TremBLrel. 21,
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                62.9%; Score 1824; DB 11; 66.4%; Pred. No. 9.9e-116; tive 31; Mismatches 80;
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Sciurognathi; Muridae;
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Query Match Best Local : Matches

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RESULTA
OPERATOR

ACC PROPERTY OF THE PROPERTY

"Expression and alternative gene (Aire).";

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J.X g of

STRAIN-B6;

SEQUENCE

FROM N.A.

Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI\_TaxID=10090;

AIRE.

Autoimmune regulator.

Submitted (FEB-1999) to the EMBL; AF128119; AAF36464.1; MGD; MGI:1338803; Aire.

MGD; MGI:1338803; Aire. InterPro; IPR000345; CytC\_heme\_bind.

InterPro; InterPro; InterPro;

IPR001841; IPR001965;

2nf\_ring.

Sp100.

Interpro; InterPro;

IPR000561; IPR000770; IPR004865;

EGF-like. SAND\_domain.

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SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia: Eutheria; Rodentia;
NCBI_TaxID=10090;
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01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruan Q.G., Wang C.Y., Shi J.D., She i "Expression and alternative splicing gene (Aire).";
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InterPro; IPR000770; SAND_domain.
InterPro; IPR004865; Sp100.
InterPro; IPR001965; Znf_PHD.
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76.6%;
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Pred. No. 1e-
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RESULT 11
ID Q9JLW
AC Q9JLW
AC Q9JLW
AC Q9JLW
DT 01-OC
DT 01-OC
DT 01-IC
DE Auto
GN AIRE
OS MUS
OC EUKA
OC MAMMI
OX NCBI
RN (1)
RP SEQI
RC STR
RA RUA
RT SEX
RT GEN
RT SUR
DR KMI
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Best Local S
Matches 277
                                                                                                                                                                                                                                                                                                                                          SMART;
SMART;
                                                                                                                                                                                                                                                                                                                PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE 405 AA; 44160 MW; 4D820E9642824F3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JLW1;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene (Aire)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-B6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Autoimmune regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JLW1
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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  245
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B); MCI:1338803; Aire.
terPro; IPR000345; Cytc_heme_bind.
terPro; IPR000770; SAND_domain.
terPro; IPR004865; Sp100.
terPro; IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                     repro; IPR000770; SANI
repro; IPR004865; Spli
repro; IPR001965; Znf.
pr00628; PHD; 1.
pr00628; PHD; 1.
pr031342; SAND; 1.
pr03172; Sp100; 1.
pr03172; Sp100; 1.
                                                                                                                                                                                                       PPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAASVQRAVTVASGDVPGTRGAVEGILIQQVFESGRSKKCIQVGGEFYTPNKFEDPSGNL
KNKARSGSSLKPVVRAKGAQGR-----DEQKVGQQCGVPPLPSLPSEPQVNQKNEDECAVC
                        KNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVC
                                                  MAASVQRAVTVASGDVPGTRGAVEGILIQQVFESGRSKKCIQVGGEFYTPNKFEDPSGNL
                                                                                                    LPPRPPTKRKALEEPRATPPATLASKSVSSPGSHLKTKPPKKPDGNLESQHLPLGNGIQT
                                                                                                                                                      SWLLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFPKDVDLNQSRKGRKPLAGPKAAV
                                                                                                                                                                    SWLLTQDSTAILDEWRVLFKDYNLERYGRLQPILDSFPKDVDLSQPRKGRKPPAVPKALV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNKARSGSSLKPVVRAKGAQVTIPGRDEQKVGQQCGVPPLPSLPSEPQVNQKNEDECAVC
                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Y., Shi J.D., alternative spl:
                                                                                                                                                                                                                                                           49.1%; Score 1424.5;
76.3%; Pred. No. 9e-1
tive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .D., She J.X.; splicing of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation
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                                                                                                                                                                                                                                                                          9e-89;
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                                                                                                                                                                                                                                                             58;
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ETP

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Matches 277
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                                                                                                                                                                                                                                                             InterPro; IPR000345; Cytc_heme_bind.
InterPro; IPR000770; SAND_domain.
InterPro; IPR004865; Sp100.
InterPro; IPR004865; Sp100.
InterPro; IPR001955; Znf_PHD.
Pfam; PF00628; PHD; 1.
Pfam; PF001742; SAND; 1.
Pfam; PF03172; Sp100; 1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
                                                                                                                                                                                                                                                                                                                            EMBL; AF128123; AAF36468.1; MGD; MGI:1338803; Aire. InterPro; IPROCOSS
                                                                                                                                                                                                                                                                                                                                              gene (Aire) ;
Submitted (FEB-1999)
                                                                                                                                                                                                                                                 PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1
SEQUENCE 408 AA; 44442 MW; 36857622FFF
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JLW2;
             363
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gene (Aire).";
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01-OCT-2000 (TremBLrel.
01-JUN-2002 (TremBLrel.
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             ETP
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                               RDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEPPV
                                                                                                                                                KNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVC
                                                                                                                           PPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQT
                                                                                                                  LPPRPPTKRKALEEPRATPPATLASKSVSSPGSHLKTKPPKKPDGNLESQHLPLGNGIQT
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                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                               408 AA; 44442 MW;
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                         C.Y.,
                                                                                                                                                                                                                       49.0%; Score 1423; 76.3%; Pred. No. 1
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15,
21,
                                                                                                                                                                                                                23; Mismatches
                                                                                                                                                                                                                                                                                                                                                               .D., She J.X. splicing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                Pred. No. 1.1e-88; 3; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Sciurognathi;
                                                                                                                                                                                                                                            36857622FFED94C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                              the mouse autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
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                        363
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Q9Y4I0
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Q9Y4I0

PRELIMINARY;

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Query Match
Best Local
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Q9JLW0;
01-CCT-2000 (TrEMBLrel. 1:
01-CCT-2000 (TrEMBLrel. 1:
01-JUN-2002 (TrEMBLrel. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00628; PHD; 1.
Pfam; PF01342; SAND; 1.
Pfam; PF03172; Sp100; 1.
SMART; SM00249; PHD; 1.
SMART; SM00258; SAND; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000345; CytC_heme_bind
InterPro; IPR000770; SAND_domain.
InterPro; IPR004865; Sp100.
InterPro; IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruan Q.G., Wang C.Y., Shi J.
"Expression and alternative
gene (Aire).";
Submitted (FEB-1999) to the
360
                         363
                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                  303
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                                                                                                             245
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                                                              RDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRABEPRPQEPPV
                                                                                                                                                           ETP
                          ETP
                                              HDGGELICCDGCPRAFHLACLSPPLQEIPSGLWRCSCCLQGRVQQNLSQPEVSRPPELPA
                                                                                                                      KNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVC
                                                                                                     KNKARSGSSLKPVVRAKGAQGR----DEQKVGQQCGVPPLPSLPSEPQVNQ-NEDECAVC
                                                                                                                                                                                                                                     PPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQT
                                                                                                                                                                                                                                                                             SWLLTQDSTAILDEWRVLFKDYNLERYGRLQPILDSFPKDVDLSQPRKGRKPPAVPKALV
                                                                                                                                                                                                                                                                                                                                     DGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKFQETLRLKEKEGCPQAFHALL
                                                                                                                                                                                                                                                                                                                                                     DAALRRLLRTEIAVAVDSAFPLLHALADHDVVPEDKFQETLHLKEKEGCPQAFHALL
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276; Conserv
                       365
                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 AA; 44032 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOCHROME_C; UNKNOWN_1.
; 44032 MW; F17D712EEC43A7CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 48.6%;
76.0%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1409;
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Sciurognathi; Muridae; Murinae; Mus
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Best Local
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Pfam; PF00385; chromo; 1.
Pfam; PF00628; PHD; 2.
Pfam; PF00628; PHD; 2.
Pfam; PF00628; CHROMO; 2.
SMART; SM00298; CHROMO; 2.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00489; HELICC; 1.
SMART; SM0049; PHD; 2.
SMART; SM00184; RING; 2.
SMART; SM00184; RING; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00598; CHROMO_1; UNKNOWN_1.
PROSITE; PS50013; CHROMO_2; 2.
PROSITE; PS00690; DEAH_ATP_HELICASE; UNKNOWN_1.
ATP-binding; Helicase.
SEQUENCE 2000 AA; 226576 MW; B085A42A5AC797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98351552; PubMed-9688266; Aubry F., Mattei M.G., Galibert F.; Aubry F., mattei of a human 17p-located snf2-like helicase family."; Eur. J. Biochem. 254:558-564(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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01-NOV-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Zinc-finger helicase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001965;
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                                                                                                                                                                               366
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                                                                                                                                                                                                                                                                                                                                                      116 PAVPKALVPPPRL-----PTKRKASEEARAAPAALTPRGTASPGSQLKAKPPKKPESSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ø9Υ4ΙΟ;
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RDDLESLLSEHTFDGILQW
                                                                                                                                                                        YTPS-----KFEDSGSGKNKARSSSG-PKPLVRAKGAQGAAPGGGEAR-LGQQGSVPAP
                       PDIPNGEWLCPRCTCPVLKGRVQKILHWRWGEPPVAVPAPQQADGNP--
                                               TSRPGTGLRCRSCSGDVTPAPVEGVL---
                                                                                               AAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAG
                                                                                                                        EGVQWEAKEEEEEYEEE------GEE-EGEKEEE----DDHMEY-----
                                                                                                                                               ATVOEVOPRAEEPRPOEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPS
                                                                                                                                                                                                                           VFQSDEGPEPEAEESDLDSGSVHSASGRPDGPVRTKKLKRGRPGRKKKKVLG----CPAV
                                                                                                                                                                                                                                                                                 KLR----
                                                                                                                                                                                                                                                                                                     EQQRLPLGNGIQTMSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKKCIQVGGEF
                                                                                                                                                                                                                                                                                                                              PSGPPALPPPPAADIQPPPIRRAKTKEGK-------GPGHKRRSKSPRVPDGRK
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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IPR002464; DEAH_box.
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IPR000330; SNF2_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000953; Chromo.
                                                                                                                                                                                                                                                                                 -GKKMAPLKIKL----
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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23.2%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 270.5;
                                              ----APSPARLAPGPAKDDTASHEPALH
                                                                      -CRVCKDGGELLCCDACISSYHIHCLNPPL
                                                                                                                                                                                                                                                                              -----GLL------GGKRK----KGGSY
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Best Local :
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Q8TDIO;
Q8TDIO;
Q8TDIO;
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TrEMBLE 21, Last annotation update)
O1-JUN-2002 (TrEMBLE 21, Last annotation update)
O1-monodomain helicase DNA binding protein 5.
time
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                    469
                                                                                                                                                     484 VEGVL----
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                                                                                               VQRILHWRWTEPPAPFMVGLPGP-----DVEPSLPPPKPLEGIPEREF--FVKWA
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                                                                                                                                                                                                   CRVCKDGGELLCCDACPSSYHLHCLNPPLPEIPNGEWLCPRCTCPPLKGK
                                                                                                                                                -APSPARLA-PGPAKDDTASHEPALHRDDLESLLSEHTFDGILQWA
                                                                                                                                                                                                                                                                                                             EE-----DDHMEF---
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Pred. No. 1.3e-08;
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Listing first 45 summaries
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seq length: 2000000000
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1: /SIDS1/gcgdata/gc
2: /SIDS1/gcgdata/gc
3: /SIDS1/gcgdata/gc
4: /SIDS1/gcgdata/gc
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Gapop 10.0 , Gapext 0.5
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1 MATDAALRRLLRHTEIAV......DGILQWAIQSMARPAAPFPS 545
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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT: *
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT: *
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982_DAT:*
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Mi-2 antigen clone	Human speckled 110	Human polypeptide	Human polypeptide	Dermatomyositis sp	A human autoimmune	A human autoimmune	Mouse AIRE protein	A human autoimmune	Human autoimmune p	Description	

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AAM93902 ABB07637 AAW57747 AAW57747 AAAW57747 AAAW571210 AAB94440 ABG11256 AAB94440 ABG11256 AAM41852 AAM41852 AAM41852 AAM41853 AAM40067 AAB601347 AAB62612 AAB671771 AAA642612 ABB71771 AAA642612 ABB71771 AAA642612 ABB71771 AAA642612 ABB9370 AAE00664 AAE202336 AAE202336 AAG31541 AAG31546	ABB71641
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## ALIGNMENTS

AAY06073	Y06073	SULT 1	
<pre>standard;</pre>			
Protein;			

545 AA.

AAY06073;

16-AUG-1999 (first entry)

Human autoimmune polyglandular disease type 1 (APGD1) protein.

Autoimmune polyendocrinopathy candidiasis ectodermal dystrophy; APECED; autoimmune polyglandular disease type 1; APGD1; AIRE; transcription factor; autoimmune disease; diagnosis; gene therapy; human.

Homo sapiens

Key

Domain Domain Region Region Region /note= "PHD zinc finger domain" /note= "putative bi-partite nuclear localisation"
131..133 /note= "putative bi-partite nuclear localisation"
299..340 113..114 Location/Qualifiers 7..11 /note= "LXXLL motif located in putative helical region, signature for nuclear receptor region, signature binding"

WO9918197-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease type 1 (APGD1 or AIRE), as predicted from a composite disease type 1 (APGD1 or AIRE), as predicted from a composite sequence (see AAX58605) of isolated cDNA clones and a PCR extension product. APGD1 protein is a transcription factor or transcription. Sequence (see AAX58605) of isolated cDNA clones and a PCR extension product. APGD1 protein is a transcription factor or transcription. Sequence of the mutated protein may prevent formation of vimentin the part of a docking mechanism regulating nuclear translocation. Aggregates of the mutated protein may prevent formation of vimentin the protein may prevent formation of vimentin with autoimmune polyendocrinopathy candidiasis ectodermal dystrophy preparation of APGD1 polypeptides. A claimed method for testing for amutation in the APGD1 gene or for a mutated form of the apgn1 columns in the APGD1 gene or for a mutated form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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02-OCT-1997;
08-OCT-1997;
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GPEGQONLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVT
                                          PVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCV
                                                         PVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCV
                                                                                                                   VCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide which co-segregates in mutated form - with camune polyendocrinopathy candidiasis ectodermal dystrophy
                                                                                                 VCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEP
                                                                                                                                                          SGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECA
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                                                                                                                                                                                                                                IQTMSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKKCIQVGGEFYTPSKFEDSG
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97EP-0117154.
97EP-0117398.
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HEALTH INST.
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Pred. No. 1.5e-211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an autoimmune regulator-1 (AIR-1) protein. The AIR polypeptides and polynucleotides can be used in methods for the diagnosis and treatment of diseases related to immune maturation and regulation of immune response towards self and nonself. They can be used particularly in the diagnosis and treatment of autoimmune polyendocrinopathy candidiasis
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           ectodermal dystrophy (APECED) (also known as autoimmune polyglandular syndrome type I (APS I)).
               121
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Peterson P,
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Shimizu N;
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Pred. No. 1.5
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02-OCT-1997;
08-OCT-1997;
    This is the amino acid an isolated cDNA clone
                           Example 20; Fig 14A-C; 77pp; English.
                                                                                                                                                                                                                                                                        Autoimmune polyendocrinopathy candidiasis ectodermal dystrophy; APECED; autoimmune polyglandular disease type 1; APGD1; AIRE; transcription factor; autoimmune disease; diagnosis; gene thera
                                                        New polypeptide which co-segregates in mutated form
                                                                                   WPI; 1999-287735/24.
                                                                                                            Aaltonen J,
                                                                                                                                (NAPU-) NAT
                                                                                                                                       (PLAC ) MAX
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                                                                                                                                                                                                                                                                                                                Mouse AIRE protein
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                                                                           AAX58606.
                                              polyendocrinopathy
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                                                                                                    Peltonen
                                                                                                            Bjorses
                                                                                                                                                         97EP-0119810.
97EP-0117154.
97EP-0117398.
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 o acid sequence of murine clone (see AAX58606). Mu
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Perheentupa J, y
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  ne AIRE,
Murine i
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Yaspo
                                              ectodermal dystrophy
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AIRE is the
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Best Local
                                                       disease; autoimmune polyendocrinopathy candidiasis ectodermal dystrophy; APECED; autoimmune polyglandular syndrome type I; APS I.
                                                                                                                      A human autoimmune regulator-2 (AIR-2) protein.
                                                                                                                                                                                                                      AAY01713 standard; Protein; 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the human AIRE (or autoimmune polyglandular disease type 1, APGDI) polypeptide (see AAY06073). The overall identity between the mouse and human AIRE proteins is 72.378. Human mutated APGDI co-segregates with autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECED). The murine homologue may be used to develop an animal model for APECED, to examine the events that lead to the development of APECED and possibly to develop agents for preventing and/or treating this autoimmune disease.
                                                                                       Autoimmune regulator-2; AIR-2; immune maturation; immune response;
                                                                                                                                                        24-JUN-1999
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Pred. No. 1.5e-143;
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WO9915559-A1 Homo sapiens

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RESULT 5
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Best Local
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   Autoimmune regulator-3; AIR-3; immune maturation; immune response; disease; autoimmune polyendocrinopathy candidiasis ectodermal dystrophy; APECED: autoimmune polygiandular syndrome type I; APS I.
                                                       A human autoimmune
                                                                               24-JUN-1999
                                                                                                                           AAY01714 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         self and nonself. They can be used particularly in the diagnosis and treatment of autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECED) (also known as autoimmune polyglandular syndrome type I (APS I)).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Peterson P,
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                                                                                                                                                                                  TFDGILQWAIQSMARPAAPFPS
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                                                      regulator-3
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Pred. No. 9.7e-100;
                                                     (AIR-3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                           Mi-2; autoantigen;
                                                                                                                                                                                                                                                                                           AAR99534
                    Homo sapiens
                                                               helicase; dermatomyositis; diagnosis
                                                                                                                                           Dermatomyositis
                                                                                                                                                                                             30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to immune maturation and regulation of immune response towards self and nonself. They can be used particularly in the diagnosis and treatment of autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECED) (also known as autoimmune polyglandular syndrome type I (APS I)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents an autoimmune regulator-3 (AIR-3) protein. The AIR polypeptides and polynucleotides can be used in methods for the diagnosis and treatment of diseases related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 32-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Autoimmune regulator 1 (AIR1) DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                    213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 GGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPG---GGEARLGQQGSVPAPL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antonarakis
Peterson P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FIIM-) FINNISH IMMUNOTECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRPGTGLRCRSCSGDVT-PAPVEGVLAPSPARLAPGPAKDDTASHEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVQEVQPRAEEPRPQEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQA
                                                                                                                                                                                                                                                                                                                                                                                                                    AE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVQEVQPRAEEPRPQEPPVETPLPPGLRSAGEEPRCQGWTP------RPCTP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CM-GVSCLCQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGVCWRPDGWGTGGQGRISGPGSMGAGQRLGSSGTQRCCWGSCFGKEVAL-RRVLHPSPV
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                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                             -MVRTCCGVLTAPLPSTGAATSQPA--PPGPGR--ACAADPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 AA;
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Scott H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----YCVW----
                                                                                                                                      specific autoantigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97FI-0003762
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                                                                                           collagen
                                                                                                                                                                                                                                                                                           Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M, Krohn K,
Shimizu N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                           disease;
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                                                                                                                                                                                                                                                                                        1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 503.5; DB 20;
Pred. No. 3.5e-30;
Pred. No. 3.5e-30;
                                                                                                                                                                                                                                                                                        ₽
                                                                                           chromosome
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                                                                                                                                        M1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VLRVSRT-----WLLVRVAGC
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                                                                                     12; 12p13;
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                                                                                                                       Query Match
Best Local
                                                                            Matches
                                                                                                                                       antigen, designated Mi-2. The sequence numbering given in the specification starts at amino acid 2, i.e. the first Met residue is omitted. The protein is hydrophilic, acidic and protruding regions of the protein are characteristic of helicases. The gene corresponding to the cDNA (AAT32301) encoding Mi-2, was localised to chromosome 12 (12p13). The DNA can be used for the recombinant production of Mi-2 which is used for, e.g. the differential diagnosis of collagen diseases, esp. dermatomyositis, e.g. by immunoassay or Western blotting.
                                                                                                                                                                                                                                                                          DNA encoding differential
                                                                                                                     Sequence
                                                                                                                                                                                                                                 The present sequence
                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-1995;
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       189 QRAVAMSSGDVPGARGAVEGILIQQVFESGG----SKKCIQVGGEFYTPSKFED--
                                                       129
                                                                                      Local
                              PFKGSSGASVAAAAAAAAVAVVESMYTATEV-APPPPPVEVPIRKAKTKEGKGPNA-----
                                                   PTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQTMSASV
                                                                                                                                                                                                                                                                                                                    1996-240280/25
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                                                                                     Similarity
                                                                                                                                                                                                                                                    Fig
                                                                                                                                                                                                                   ent sequence is that of a 218 kD dermatomyositis specific auto-
designated Mi-2. The sequence numbering given in the
                                                                                                                                                                                                                                                                                                                                          Seelig
                                                                                                                     1911 AA;
                                                                           Conservative
                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                         dermatomyositis specific auto:antigen - useful diagnosis and treatment of dermatomyositis
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1121..1144
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943..9
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/note= "contains
747..758
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257..287
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133..143
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/note= "contains 3
                                                                                     8.3%;
23.1%;
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                                                                                    Score
Pred.
                                                                           Mismatches
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                                                                        No. 3.3e-09;
smatches 172;
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14-SEP-2000;
19-OCT-2000;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                               N-PSDB;
                                                                                                              Zhao
                                                                                                                                Tang
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                                               nucleic acids and polypeptides, useful secontral nervous.system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTPAPVEGVL-----APSPARL-APGPAKDDTASHEPALHRDDLESLLSEHTFDGILQW
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                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide
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Wang i
Zhou
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2000US-0552317.

2000US-0598042.

2000US-0620312.

2000US-0653450.

2000US-0652191.

2000US-0693036.

2000US-0693036.
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Wehrman T, )
Goodrich R,
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a AJ,
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Zhang
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The invention relates to the encoded polypeptides

human nucleic acids (AAI57798-AAI61369) (AAM38642-AAM42213) with nootropic,

Example

4; SEQ ID NO 2433; 10078pp;

English.

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Best Local
                                                                                                                                    peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral solerosis; Shy-Drager Syndrome; chemotactic; chemokineito; through little 3.
                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; peripheral nervous system; neuropathy; central nervous system;
                                              WO200153312-A1
                                                                             Homo sapiens.
                                                                                                                           chemokinetic;
                                                                                                                                                                                                                         Human polypeptide
                                                                                                                                                                                                                                                         22-OCT-2001
                                                                                                                                                                                                                                                                                                                       AAM41074 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                             ALKGKVQKILIWKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVK---WQGMSYW 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                       VTPAPVEGVL - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVSDGSTSRSRKKLRTTK-----KKKKGEE-EVTAVDGYETD------HQDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders
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97; Conserv
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                                                                                                                          thrombolytic;
                                                                                                                                                                                                                       SEQ ID NO
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; Pred. No. 3.3e-09;
51; Mismatches 172;
                                                                                                                     drug screening;
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                                                                                                                      arthritis;
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Best Local
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25-APR-2000;
09-JUL-2000;
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19-OCT-2000;
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    VTPAPVEGVL - - -
                                                                                                                                                          EPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLL
                                                                              CVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGD
                                                                                                                                                                                                        CEVCQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEK---EGIQWEAKED---
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                                                                                                                        -RRKPKGSPRVPDAKKPKPKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSY
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Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1936 AA;
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--APSPARL-APGPAKDDTASHEPALHRDDLESLLSEHTFDGILQW
                                        CRVCKDGGELLCCDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCP
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Pred. No. 3.4e-09;
1; Mismatches 172;
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531

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ABB07636
В
                                                                                                                                                                                                                                                                                                                                                                      Sp110; speckled 110; nuclear body; gene transcription; dimerisation; nuclear hormone receptor; primary biliary cirrhosis; PBC; human; cell differentiation; cellular defence; cytostatic; anorectic;
                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                 Human speckled 110
                                                                                                                                                                                                                                                                                                                                                                                                              20-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                           ABB07636
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB07636 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                              24-JUL-2001; 2001WO-US23248
                                                                                                                                                                                                                                                                       WO200208383-A2.
                                                                                                                                                                                                                                                                                            Doma in
                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                  (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                 24-JUL-2000; 2000US-220305P
                                                                                                                                                                                                                                                           31-JAN-2002.
                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 ALKGKVQKILIWKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVK---WQGMSYW
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                       /note= ".
537..577
                                                                                                                                                                                                                                                                                           /note=
606..67
                                                                                                                                                                                                                                                                                                                     454..532
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                  (Spl10) polypeptide.
                                                                                                                                                                                                                                                                                             . 67
                                                                                                                                                                                                                                                                                                 "plant homeobox
                                                                                                                                                                                                                                                                                     "bromodomain"
                                                                                                                                                                                                                                                                                                                           "Sp100-like domain"
                                                                                                                                                                                                                                                                                                              "SAND domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                         689
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Novel substantially pure polypeptide component of the nuclear body speckled 110, useful in screening methods, in clinical diagnostic methods, and for treating myeloid malignancies, inflammation and

Bloch DB,

Bloch KD;

N-PSDB;

2002-227042/28 ABA95062.

Claim Fig 2; 55pp; English.

compound that modulates (i) SpillO dimerisation; (ii) SpillO binding to a nuclear hormone receptor; (iii) binding of an SpillO dimer to an SpillO-binding nucleotide sequence and in a screening method for identifying a polypeptide that dimerises with SpillO to form a constitutively active or hyperactive or inactive heterodimer. It is useful for diagnosing primary biliary cirrhosis (PBC) and is also useful for producing SpillO-specific antibodies, for inhibiting viral replication and facilitating differentiation of cells, e.g. myeloid cells, and activation of cells involved in host defence, to treat myeloid malignancies, to enhance cellular defence mechanisms, to treat inflammation, to achieve alteration in lipid profiles, to block estrogen receptors in treatment estrogen responsive tumours, and for treating obesity. The present sequence represents the human SpillO polypeptide. The invention relates to cloning and characterisation of a cDNA encoding Sp110 (speckled 110), a novel 110 kDa polypeptide component of the nuclear body. The Sp110 polypeptide comprises a Sp100-11ke domain, a SAND domain, a plant homeobox domain, and a bromodomain. Sp110 functions as an activator of gene transcription and serves as a nuclear hormone receptor co-activator. Sp110 is useful in screening for identifying a compound that modulates (i) Sp110 dimerisation; (ii) Sp110 binding to a

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RESULT 10
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116
07-SEP-1990;
                        05-SEP-1991;
                                                                           WO9204472-A
                                                                                                  Homo sapiens
                                                                                                                            syndrome;
                                                                                                                                        Myositis-specific antigen;
                                                                                                                                                                 Mi-2 antigen clone L1 encoded
                                                                                                                                                                                            27-JUL-1992
                                                                                                                                                                                                                                             AAR22280 standard; Protein; 351 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 DPVLPLPALIQEGRSTSVTNDKLTSKMNAEEDSEEMPSLLTSTVQVASDNLIPQIRDKED
                                                                                                                                                                                                                                                                                                             569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358
                                                                                                                                                                                                                                                                                                                                      332 SGTWRCSSC
                                                                                                                                                                                                                                                                                                                                                                                         272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 PRGTASP--GSQLKAK-----PPKKPESSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 POAFHALLSWILITODSTAILDFWRVLFKDYNLERYGRLOPILDSFPKDVDLSOPRKGRKP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ATDAALRELLRIHRTEIAVAVDSAFPLLHALADHDVVPEDKFQETLHLKEKEGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAV-----PKALVPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRVVHNILTQL---ERTFNLSLLVTLFSQINLREYPNLVTIYRSF-KRVGASYERQSRDT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMEEALFQHFMHQKLGIAYAIHKPFPFFEGLLDNSIITKRMYMESL----EACRNLIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILLEAPTGLAEGSSLHTPLALPPPQPPQPSCSPCAPRVSEPGTSSQQSDEILSESPSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EQQRLPL-----GNGIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSTPSDKKGKKRKRCIWSTPKRRHKKKSL
                                                                                                                                                                                                                                                                                                             RMLWSCTFC
                                                                                                                                                                                                                                                                                                                                                                                      RLGQQGSVPAPLALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIP 331
                                                                                                                                                                                                                                                                                                                                                                                                                                          QVFESGGSKKCIQ-VGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCARKSRSKEKKKEKDICSSSKRRFQKNIHRRGKPKSDTVDFHCSKLPVTCGEAKGILYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNEGKRSQKTPSTPRRVTQGAASPGHGIQEKLQVVDKVTQRKDDSTWNSEVMMRVQKART
                                                                                                                                                                                                                                                                                                                                                                TLGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                   KKMKHGSSVKCIRNEDGTWLTPNEFEVEGKGRN----AKNWKRNIRCEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRGTASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -PRLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            689
                                                                                                                          specific antigen; polymyositis scleroderma overlap; dermatomyositis; autoantibodies; immunodiagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                               577
90US-0579023
                         91WO-US06418
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                                                                                                                                                                                                                                                                                                                                                                44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 238; DB 23; Pred. No. 1.6e-09;
                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -VAMSSGDVPGARGAVEGILIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TMSASVQRA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
Drosophila; developmental biology; cell signalling; insecticide;
                                    Drosophila melanogaster polypeptide SEQ ID NO 41715.
                                                                              26-MAR-2002 (first entry)
                                                                                                                    ABB71641;
                                                                                                                                           ABB71641 standard; Protein; 884 AA
                                                                                                                                                                                                                         240 VPPPRPLQGRSEREFFVK---WVGLSYW 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kb and includes a single long open reading frame spanning the entire insert, in phase with beta galactosidase. Since there are no start or stop codons, the insert does not contain the entire gene. The clone may be used as a DNA probe to isolate DNA encoding additional portions of the human antigens. This DNA and the protein encoded by expressing anti-Mi-2 autoantibodies, and to diagnose dermatomyositis.
                                                                                                                                                                                                                                                          504 TASHEPALHRDDLESLLSEHTFDGILOW 531
                                                                                                                                                                                                                                                                                                     183
                                                                                                                                                                                                                                                                                                                454 HWRCHFPAGTSRPGTGLRCRSCSGDVTPAPVEGVL-----APSPARLAPGPAKDD 503
                                                                                                                                                                                                                                                                                                                                                                                394 YKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAAAF 453
                                                                                                                                                                                                                                                                                                                                                                                                               121 KWSCPHCEKEGVQWEAKEEEEEEYEEE-----GEE-EGEKEEE-----DDHME 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                      162
                                                                                                                                                                                                                                                                                                                                                                                                                                               334 TWRCSSCLOATVOEVQPRAEEPRPQEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from normal controls or from dermatomyositis patients contg. auto-antibodies other than anti-Mi-2. Clone L1 was used to screen sera from 40 patients. The cDNA was expressed. The insert was 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E. coli 11090 and was screened with serum from a deratomyositis patient. This serum had previously been found to only contain anti-M1-2 autoantibodies. A cDNA clone L1 was selected that expressed a protein which reacted with the anti-M1-2 serum but not with the sera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 GOOGSVPAPLALPSDPQLHQKNEDECAYCRDGGELICCDGCPRAFHLACLSPPLREIPSG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 GGSKKCIQVGGEFYTPSKFE---DSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEAR-L 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A human thrombocyte lambda gt 11 expression library was expressed in E. coli Y1090 and was screened with comm factoring was expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Fig 1; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding myositis-specific antigen Mi-2 - useful in diagnosing dermatomyositis and polymyositis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 G----CPAVAGEEEVDGYETDHQDYCEVCQQGGEIILCDTCPRAYHLVCLDPELDRAPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-114375/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ22728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Targoff IN;
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                                                                                                                                                                                                                                                                                  HIHCLNPPLPDIPNGEWLCPRCTCPVLKGRVQKILHWRWGEPPVAVPAPQQADGNP----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGKRKKGGSSDEGPEPEAEESDLDSGSVHSASGRPDGP---VRTKKLKRGRPGRKKKKVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.1%; Score 236.5; DI
25.6%; Pred. No. 8.9e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 351;
                                                                                                                                                                                                                                                                                                                                                   --CRVCKDGGELLCCDACISSY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
453 FCLNPPLDTIPDGDWRCPRCS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics in higher eukaryotes for the development of discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPC at the company of the company of the printed specification, but was obtained in electronic format directly from WIPC at the company of the company of the printed specification.
                                                                                                                                    408
                                                                                 396 HLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHW 455
                                                                                                                                                336 RCSSCLQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYK 395
                                                                                                                                                                                                  276 QGSVPAPLALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTW 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                 220
                                                                                                                                                                                                                                                                                                                                             160 AKPPKKPESSAEQQRLPLGNGIQTMSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGG
                                                                                                                                                                                                                                                                                                               295 ERMLQKSDDSADEKEAPVS-----SKADNSAPAA-----
                                                                                                                                                                                                                                                                                                                                                                            251 KKGRRPSG------KVPTLKIKLLGKRKRDSSDEEQDAS------GASERDSDLEF 294
                                                                                                                                                                                                                                                                                                                                                                                                            110 RKGRKPPAVPKALVPPPRLPT-----KRKASEEARAAAPAALTPRGTASPGSQLK- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 41715; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                              RCHFPAGTSRPGTGLRCRSCS 476
                                                                                                                       SCPHC----EADGGAAEEEDDDEHQEF-----
                                                                                                                                                                                  KNKLKKTKNFPEGEDGEHEHODYCEVCQOGGEIILCDTCPRAYHLVCLEPELDEPPEGKW
                                                                                                                                                                                                                                                -----APVVRKK-----AKTKIGNKEKK 347
                                                                                                                                                                                                                                                                              SKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLG----Q 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         884 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                              7.8%; Score 227; DB 22; 20.2%; Pred. No. 1.5e-08; tive 39; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers
                                                      -- CRVCKDGGELLCCDSCPSAYHT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                    407
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                                                                                                                                                                                                                                                                                                                                       RESULT 12
AAM93902
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                           Matches
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                           molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID NO 4045; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM93902 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-2000; 2000EP-0114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM93902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST
                                                                                                                                                                                    131
283 LALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQ 342
                                                                                                                                                                                                             631 STIMLD--NIVRKDTNID-HGQPRPPSNRTVQSPNSSVPSPGLAGPVTMTSVHPPIRSPS 687
                                                                                                                                                                                                                                                                                           rocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primers useful for synthesizing full length cDNA clones in genetic manipulation - \,
                                                                                                                                                                               KRKASEEARAAAPAALTPRGTASPG------SQLKAKPPKK-----PESSA 170
                                                                                                                     EQQRLPLGNGIQTMSASVQRAVAMSS------GDVPGARGAVEGILIQQVFESGGSKK 222
                                                                                                                                                   --ASSVGSRGSSGSSSKPAGADSTHKVPVVMLEPIRIKQENSGPPENYDFPVVIVKQESD 745
                                                                                                                                                                                                                                           STAILDFWRVLFKDYNLERYGRLQPILDSFPKDVDLSQPRKGRKPPAVPKALVPPPRLPT 130
                                                          CIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAP
                                                                                        EESRPQNANYPRSILTSLLLNSSQSSTSEETVLRSDAPDSTGDQPGL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-524255/58.
                                                                                                                                                                                                                                                                         1 Similarity
77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Þ
                                                                                                                                                                                                                                                                                                                                     1050 AA;
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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2000JP-0183765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0194486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 1050
                                                                                                                                                                                                                                                                                       24.6%;
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ma T, Nagai
                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                      Score 227; DB 22;
Pred. No. 1.8e-08;
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                                                                                                                                                                                                                                                                         Mismatches
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K, Kojima
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                                                                                                                                                                                                                                                                         104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Otsuki
                                                                                                                                                                                                                                                                                                    Length 1050;
                                                                                                                                                                                                                                                                         Indels
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T, Koga
                                                                                                                                                                                                                                                                        86;
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                                                                                                                                                                                                                                                                      Gaps
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                                              CC The invention relates to cloning and characterisation of a cDNA encoding CC Spl10 (speckled 110), a novel 110 kDa polypeptide component of the CC nuclear body. The Spl10 polypeptide comprises a Spl00-like domain, a CC SAND domain, a plant homeobox domain, and a bromodomain. Spl10 functions CC receptor co-activator. Spl10 is useful in screening for identifying a CC compound that modulates (i) Spl10 dimerisation; (ii) Spl10 binding to a conclear hormone receptor; (iii) binding of an Spl10 dimer to an Spl10-cc binding nucleotide sequence and in a screening method for identifying a CC polypeptide that dimerises with Spl10 to form a constitutively active or hyperactive or inactive heterodimer. It is useful for diagnosing primary CC bilary cirrhosis (PBC) and is also useful for producing Spl10-specific cantibodies, for inhibiting viral replication and facilitating cC differentiation of cells, e.g. myeloid cells, and activation of cells cells, e.g. myeloid cells, and activation of cells cellular defence mechanisms, to treat myeloid malignancies, to enhance CC cellular defence mechanisms, to treat inflammation, to achieve cellular defence mechanisms, to treat inflammation, to achieve the nuclear body.

CC sequence represents the human Spl40 polypeptide, which recruits Spl10
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel substantially pure polypeptide component of the nuclear body, speckled 110, useful in screening methods, in clinical diagnostic methods, and for treating myeloid malignancies, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sp110; speckled 110; nuclear body; gene transcription; dimerisation; nuclear hormone receptor; primary biliary cirrhosis; PBC; human; Sp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB07637 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bloch DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2000; 2000US-220305P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell differentiation; cellular defence; cytostatic; anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human speckled 140 (Sp140) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB07637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            873 LSKPEVEYDCDAP 885
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                                      the nuclear body.
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Query Match Best Local Matches 128;

Similarity

7.6%; Score 220.5; DB: 20.5%; Pred. No. 3.7e-08

DB 23;

Conservative

53;

Mismatches 152;

Indels Length 753;

291;

Gaps

24;

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RESULT 14
AAW57747
ID AAW57
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         Bloch DB,
                                                                                       02-OCT-1997;
                                                                02-OCT-1996;
                                                                                                             09-APR-1998
                               (BLOC/) BLOCH
                                                                                                                                  W09814569-A1
                                                                                                                                                         Homo sapiens
                                                                                                                                                                             Sp140; leukocyte specific autoimmune disease; viral
                                                                                                                                                                                                            Leukocyte specific protein, Sp140
                                                                                                                                                                                                                                   17-SEP-1998 (first entry)
                                                                                                                                                                                                                                                             AAW57747;
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                                                                                                                                                                                                                                                                                                                                           622
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                                                                                                                                                                                                                                                                                                                                       KESPGSQQCCQESEVLERQMCPEE 645
                                                                                                                                                                                                                                                                                                                                                                              NNSSVDPCM--RNLDECEVCRDGGELFCCDTCSRVFHEDCHIPPV-EAERTPWNCIFCRM 621
                                                                                                                                                                                                                                                                                                                                                                                                    --- PSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSC--
                                                                                                                                                                                                                                                                                                                                                                                                                          KG---GHARSKNW-RLSVRC------GGWPLRWLMENGFLPDPPRIRYRKKKRILKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSRASRKHKDETVDFKAPLLPVTCGGVKGILHKKKLQQGILVKCIQTEDGKWFTPTEFEI 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEKCSCVMCFSEEVPGSPEARTESDQACGTMDTVDIANNSTLGKPKRKRRKKRGHGWSRM
                                                                                                                                                                                                                                                                                                                                                             -----LQATVQEVQPRAEEPRPQE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                         SGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEAR-LGQQGSVPAPLAL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RMRRQKNSQQNDNSKADGQVVSSEKKANVNLKDLSKIRGRKRGKPGTRFTQSDRAAQKRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -IQTMSASVQRAVAMSSGDV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRRLLRLHRTEIAVAVDSAFPLLHALADHDVVPE---DKFQETLHLKEKEGCPQAFHALL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWLLTQDSTAILDFWRVLFKDYNLERYGRLQPILDSF-----
         Bloch KD,
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                               × D
                                                                96US-0027347
                                                                                      97WO-US17715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GAVEGILIQQVFESGGSKKCIQV-GGEFYTPSKFED
                                                                                                                                                                            infection; cancer.
                                                                                                                                                                                    protein; gene transcription regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QQRLPLGNG----
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   624
                                 341
                                                                 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis, systemic lupus erythematosus, Sjogren's syndrome, scleroderma and multiple sclerosis, viral diseases including those caused by herpes simplex virus, cytomegalovirus, HIV, hepatitis virus, human T-cell leukaemia virus-1 (HTLV-1) and adenovirus, and cancers including leukaemias, particularly acute promyelocytic leukaemia, cancers of the breast, ovary, prostate, bone, liver, pancreas or spleen, sarcomas and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the leukocyte specific protein, Sp140 of the invention. The Sp140 polypeptides act as gene transcription regulators. They can be used to develop products for use in the diagnosis and treatment of autoimmune diseases such as primary biliary cirrhosis,
                                                                                                                                519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated gene transcription regulator, \mbox{Sp140} - used products for the diagnosis and treatment of auto-immune viral infections or cancers
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                                                                                                                                                               241
                                                                                                                                                                                                459
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                                                                                                                                                                                                                                                                                                                                                                                                                                               219 VSCKLAIQIDEGESEEMPKLLPYDTEETFDLKTPQVTNEGEPEKGLCLLPGEGEEGSDDC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 L---EKTFGWSHLEALFSRINLMAYPDLNEIYRSFQNVCYEHSPLQMNNVNDLEDRPRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV24559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 RLLRLHRTEIAVAVDSAFPLLHALADHDVVPE---DKFQETLHLKEKEGCPQAFHALLSW 65
SPGSQQCCQESEVLERQMCPEE
                                                        SSVDPCM--RNLDECEVCRDGGELFCCDTCSRVFHEDCHIPPV-EAERTPWNCIFCRMKE
                                                                             -PSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSC----
                              ---LQATVQEVQPRAEEPRPQE 359
                                                                                                                      ---GHARSKNW-RLSVRC------GGWPLRWLMENGFLPDPPRIRYRKKKRILKSQNN
                                                                                                                                                      SGKNKARSSSGPKPLVRAKGAQGAAPGGGEAR-LGQQGSVPAPLAL-------
                                                                                                                                                                                      RASRKHKDETVDFKAPLLPVTCGGVKGILHKKKLQQGILVKCIQTEDGKWFTPTEFEIKG
                                                                                                                                                                                                                                                    RRQKNSQQNDNSKADGQVVSSEKKANVNLKDLSKIRGRKRGKPGTRFTQSDRAAQKRVRS
                                                                                                                                                                                                                                                                                         QTMSASVQRAVAMSSGDV-----
                                                                                                                                                                                                                                                                                                                  KCSCVMCFSEEVPGSPEARTESDQACGTMDTVDIANNSTLGKPKRKRRKKRGHGWSRMRM
                                                                                                                                                                                                                                                                                                                                                                                 SEMCDGEERQEASSSLARRGSVSSELENHPMNEEGESEELASSLLYDNVPGAEQSAYENE 338
                                                                                                                                                                                                                                                                                                                                                                                                                      ----EARAAAPAALTPRGTAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYGKQENSNACHEMDDIAVPQEALSSSARCEPGFSSESCEQLALPKAGGGDAEDAPSLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLTQDSTAILDFWRVLFKDYNLERYGRLQPILDSF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFFRENKVEIASAITRPFPFLMGLRDRSFISEQMYEHFQEA--FRNLVPVTRVMYCVLSE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             753 AA;
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                                                                                                                                                                                                                                                                                                                                                          -KPPKKPESSAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PPRLP-----TKRKASE----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DLSQPRK-----GRKPP-----AVPKA------LVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.48;
                                                                                                                                                                                                          ---GAVEGILIQQVFESGGSKKCIQV-GGEFYTPSKFEDSG
645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 213.5; DB 19;
Pred. No. 1.3e-07;
34; Mismatches 148;
                                                                                                                                                                                                                                                                                       -PGAR--
                                                                                                                                                                                                                                                                                                                                                   -- QQRLPLGNG----I 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 753;
                                                                                                                                                                                                                                                                                                                                                                                                                   -PGSQLKA---- 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to develop diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291;
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                                                          623
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ABG11257
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                                                                                                                                                                    Matches 129;
                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                           (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in reating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #11248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG11257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG11257 standard; Protein; 771 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 41616; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                    Sequence
105 L---EKTFGWSHLEALFSRINLMAYPDLNEIYRSFQNVCYEHSPLQMNNVNDLEDRPRLL 161
                                       66 LLTQDSTAILDFWRVLFKDYNLERYGRLQPILDSF-----
                                                                               47
                                                                                                                                                                                        Local Similarity
                                                                                                                       9 RLLRLHRTEIAVAVDSAFPLLHALADHDVVPE---DKFQETLHLKEKEGCPQAFHALLSW 65
                                                                               RFFRENKVEIASAITRPFPFLMGLRDRSFISEQMYEHFQEA--FRNLVPVTRVMYCVLSE 104
                                                                                                                                                                                                                                                    771 AA;
                                                                                                                                                                    Conservative
                                                                                                                                                                                   7.4%; Score 213.5; DB 22; 20.7%; Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                                                                                                               54; Mismatches 148; Indels 291; Gaps
                                          -----PKDV 104
                                                                                                                                                                                                         Length 771;
                                                                                                                                                                    26;
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	SPGSQQCCQESEVLERQMCPEE 648	627	Db
	LQATVQEVQPRAEEPRPQE 359	341	Qy
AERTPWNCIFCRMKE 626		570	Db
IPSGTWRCSSC 340	-PSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSC-	286	Qy
IRYRKKKRILKSQNN 569	GHARSKNW-RLSVRCGGWPLRWLMENGFLPDPPRIRYRKKKRILKSQNN	522	Дb
L 285	SGKNKARSSSGPKPLVRAKGAQGAAPGGGEAR-LGQQGSVPAPLAL-	241	Qy
EDGKWFTPTEFEIKG 521	RASRKHKDETVDFKAPLLPVTCGGVKGILHKKKLQQGILVKCIQTEDGKWFTPTEFEIKG	462	DЬ
-GGEFYTPSKFEDSG 240		204	Qy
RFTQSDRAAQKRVRS 461	RRQKNSQQNDNSKADGQVVSSEKKANVNLKDLSKIRGRKRGKPGTRFTQSDRAAQKRVRS	402	Db
R 203	QTMSASVQRAVAMSSGDVPGAR-	182	Qy
KRRKKRGHGWSRMRM 401	KCSCVMCFSEEVPGSPEARTESDQACGTMDTVDIANNSTLGKPKRKKRGHGWSRMRM	342	Db
-QQRLPLGNGI 181		161	Qy
YDNVPGAEQSAYENE 341	SEMCDGEERQEASSSLARRGSVSSELENHPMNEEGESEELASSLLYDNVPGAEQSAYENE	282	рb
PGSQLKA 160	EARAAAPAALTPRGTAS	137	Qy
LCLLPGEGEEGSDDC 281	VSCKLAIQIDEGESEEMPKLLPYDTEETFDLKTPQVTNEGEPEKGLCLLPGEGEEGSDDC	222	DЬ
136	PPRLPTKRKASE	125	Qy
KAGGGDAEDAPSLLP 221	PYGKQENSNACHEMDDIAVPQEALSSSARCEPGFSSESCEQLALPKAGGGDAEDAPSLLP	162	DЬ
KALVP 124	ALSQPRKGRKPPAVPKA-	105	Qy

Search completed: March 13, 2003, 17:52:52 Job time: 43 secs

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Post-processing: Minimum Match 0%
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
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                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        March 13, 2003, 17:54:02; Search time 17 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                            /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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SUMMARIES
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1477.658 Million cell updates/sec
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17 143	114	16 143	15 145.5	14 147.5	13 147.5	12 147.5	11 148.5	10 149	9 151.5	8 153	7 155	6 156	5 159.5	4 165	3 166	2 168	1 168	Result No. Score
4 4 0 0	4.9	4.9	5.0	5.1	5.1	ر. ب	5.1	5.1	5.2	5. 3	ω	5.4	5.5	5.7	5.7	5.8	5.8	Query Match
510 1274	527	527	1251	538	538	538	386	601	2462	1207	1400	432	1023	167	549	1237	1134	Query Match Length
9 10	10	9	9	12	12	9	10	10	9	9	10	10	9	9	10	10	9	DB
US-09-866-562-56 US-10-020-215-2	US-09-738-973-216	US-09-854-133-216	US-10-189-971-16	US-10-023-523-43	US-10-023-529-43	US-09-976-740-43	US-09-764-176-3	US-09-925-301-844	US-09-819-104A-5	US-10-189-971-20	US-09-764-176-7	US-09-764-864-1184	US-09-893-519A-14	US-10-005-057A-31	US-09-764-864-1254	US-09-862-027-78	US-09-836-392-16	ID
Sequence 56, Appl	Sequence 216, App	Sequence 216, App	Sequence 16, Appl	Sequence 43, Appl	Sequence 43, Appl	Sequence 43, Appl	Sequence 3, Appli	Sequence 844, App	Sequence 5, Appli	Sequence 20, Appl	Sequence 7, Appli	Sequence 1184, Ap	Sequence 14, Appl	Sequence 31, Appl	Sequence 1254, Ap		Sequence 16, Appl	Description

5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	0.7
131	131	131.5	131.5	133	133.5	133.5	133.5	134	134	134	134	134	134	134	134	134.5	135	135	135.5	136	139	139	139	139.5	140
4.5	4.5	4.5	4.5	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.8	4. o
4019	4019	1690	420	1317	1002	1002	1002	1628	1593	1570	1535	1512	1477	1342	1192	693	846	524	2441	522	550	550	550	1056	1007
10	9	10	10	10	10	10	9	9	9	9	9	9	9	9	9	9	10	9	12	9	12	12	9	9	٧
US-09-738-973-425	US-09-854-133-425	US-09-788-043C-5	US-09-764-864-1084	US-09-963-896-7	US-09-812-633-3	US-09-812-471-3	US-09-988-117-3	US-10-189-971-2	US-10-189-971-4	US-10-189-971-12	US-10-189-971-14	US-10-189-971-10	US-10-189-971-8	US-10-189-971-24	US-10-189-971-18	US-10-029-217A-4	US-09-858-664A-3	US-09-764-868-761	US-10-109-886-8	US-09-764-868-1138	US-10-023-523-47	US-10-023-529-47	US-09-976-740-47	US-10-161-510-10	OS-09-BIY-IU4A-Z
Sequence 425, App	Sequence 425, App	Sequence 5, Appli	Sequence 1084, Ap	Sequence 7, Appli	Sequence 3, Appli	ω ω	Sequence 3, Appli	2		12,		10	8	Sequence 24, Appl	Sequence 18, Appl	Sequence 4, Appli	Sequence 3, Appli	Sequence 761, App	Sequence 8, Appli		Sequence 47, Appl	Sequence 47, Appl	Sequence 47, Appl	Sequence 10, Appl	sequence 2, Appli

## ALIGNMENTS

RESULT 1 US-09-836-392-16

Sequence 16, Application US/09836392 Patent No. US20020173458A1

GENERAL INFORMATION: APPLICANT: Ruben et al.

TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides TITLE OF INVENTION: Antibodies

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                                                 Qy
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                                                                                                                                                                                                                                                               Qγ
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PRIOR APPLICATION NUMBER: PCT/US00/28066
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/159,542
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/189,027
PRIOR APPLICATION NUMBER: 60/189,027
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
SEQ ID NO 16
LENGTH: 1134
TYPE: PRT
                                                                                                                                                                                                                                                                                                                    Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PT020P1
CURRENT APPLICATION NUMBER: US/09/836,392
CURRENT FILING DATE: 2001-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
884 LG---APRQVAVRRLGRQESPLSLGADPLL-PEGASRPPVSSKEKESPGGAEACTPPRAT 939
                                                                                                                                                                                                      767 PLSPLAHTPSPTQASPPPLPGHTVGSSHTTQSFPAKLHSSPPVVRPRPKSAEPPRSPLLK 826
                                                                                                                                                                                                                                                             116 PAVPKALVP-----PPRLPTKRKASEEARAAPAALTPRGTASPGSQLKAKPPKKPESS 169
                                            227 GGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGA-----QGAAPGGGEARLGQQGS 278
                                                                                                   827 RVQSAEKLG----ASLSADKKGALRKHSLEVGHPDFRKDFHGELALHSLAESDGETPPVEG
                                                                                                                                                    170 AEQORLPLGNGIQTMSASVQRAVAMSSGDV--PGARGAVEG-ILIQQVFESGGSKKCIQV 226
                                                                                                                                                                                                                                                                                                                 5.8%; Score 168; DB 9; Length 1134; 26.4%; Pred. No. 0.01; ative 41; Mismatches 180; Indels 8
                                                                                                                                                                                                                                                                                                                    Indels 88;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 78, Application US/09862027 Patent No. US20020142428A1 GENERAL INFORMATION:
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TITLE OF INVENTION: No. US20020142428A1e1 Kinases and Uses Thereof FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: uS/09/862,027
CURRENT FILING DATE: 2001-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/345,473 PRIOR FILING DATE: 1999-06-30 NUMBER OF SEQ ID NOS: 82
                                                          1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                        1149 LEVVEERTTLSGPRSKPASPKLSPEP--QTPSLAPAKCSAPSSAVTPVPPA--SLLGSGT
                                                                                                                                                                                                      1090 RSSSGEAGTPLVPIVVEPARPGAKAV-VPQPLGADSKGLQEPAPLAPSVPEAPRGRERWV 1148
                                                                                                                                                                                                                                                                                   1043 TPGGRTLERDVGCTRHQSVQTE-----DG-----TGGMARAVAKAALS-PVQEHETG--R 1089
                                                                               442 DVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAPV--ECVLAPSPARLAPGP 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                           337 CSSCLQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGEEVRGP--PGEPLA--GMD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 AEQORLPLGNGIQTMSASVQRAVAMSSGDV--PGARGAVEG-ILIQQVFESGGSKKCIQV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            870 PLSPLAHTPSPTQASPPPLPGHTVGSSHTTQSFPAKLHSSPPVVRPRPKSAEPPRSPLLK 929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 DVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAPV--EGVLAPSPARLAPGP 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                        VPAPLALPSDP--QLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWR 336
                                                                                                                                                                                                                                                                                                                                                                LG---APRQVAVRRLGRQESPLSLGADPLL-PEGASRPPVSSKEKESPGGAEACTPPRAT 1042
                                                                                                                                                                                                                                                                                                                                                                                                        GGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGA-----QGAAPGGGEARLGQQGS
                                                                                                                                                              -----TTLV-YKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGT 441
                                                                                                                                                                                                                                                                                                                                                                                                                                               RVQSAEKLG---ASLSADKKGALRKHSLEVGHPDFRKDFHGELALHSLAESDGETPPVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPGGRTLERDVGCTRHQSVQTE-----DG-----TGGMARAVAKAALS-PVQEHETG--R 986
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26.4%;
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                                         ----KPQVGLTSRCPAEAVPPAGLTKKGVSSPAP----PGP 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 168; DB 1; Pred. No. 0.011; 41; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1237;
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US-09-164-864-1254

APPLICANT: Rafaľski, Antoní J.
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Klein, Ted M.
TITLE OF INVENTION: Transcriptional Regulator Nucleic Acids,
TITLE OF INVENTION: Polypeptides and Methods of Use Thereof
FILE REFERENCE: 1288

APPLICANT:

Danilevskaya, O Mahajan, Pramod

olga

CURRENT APPLICATION NUMBER: US/10/005,057A

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RESULT 4
US-10-005-057A-31
; Sequence 31, Application US/10005057A
; Patent No. US20020170087A1
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   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                   APPLICANT: Tao, Yumin APPLICANT: Gordon-Ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1254, Application US/09764864 Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prior application data removed NUMBER OF SEQ ID NOS: 1792
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TYPE: PRT
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (464)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (297)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (290)
                                                                                                                                                                                   542 LLSFP 546
                                                                                                                                                                                                                   327
                                                                                                                                                                                                                                              493 -HRSARIGGDGN---
                                                                                                                                                                                                                                                                                                       433 SPESSLTPPLSTNLHLESELDALASLENHVKXEPADMNESCKQSGLSSLVNGKSPIRSLM 492
                                                                                                                                                                                                                                                                                                                                                                                    376
                                                                                                                                                                                                                                                                                                                                                                                                      175 LPLGNGIQTMSASVQRAVAMSSGDV-----PGARGAV---EGILIQQVFESGGSKKCIQV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 PPAVPKALVPPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                               334 PPQPTSTMNPSP--
                                                                                                                                                                                                                                                                                                                                       GGE-----SSSGPKPLVRAKGAQGAAP
                                                                                                                                                                                                                                                                                                                                                                        GSCGSSGRT---AEKTSLSFKSDQVKVKQEPGTEDEICSFSGGVKQEKTEDGRRSACMLS
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                                                                                                                                                                                                                                                              61;
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(21)
   Lowe,
                 Shen,
                                Gordon-Kamm, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
Keith S.
                    ВО
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 166; DB 10;
Pred. No. 0.0062;
1; Mismatches 93;
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APPLICANT: DAVIDOY, Eugene
APPLICANT: DAVIDOY, Eugene
FILE OF INVENTION: ANTIFUNGAL COMPOUNDS AND MET
FILE REFERENCE: 0342/16548-US2
CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR APPLICATION NUMBER: US 60/224,457
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 14
LENGTH: 1023
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US-10-005-057A-31
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                                                                                                                     Query Match 5.5%; Score 159.5; DI Best Local Similarity 23.2%; Pred. No. 0.03; Matches 109; Conservative 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.7%;
Best Local Similarity 55.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ANADYS PHARMACEUTICALS, INC.
APPLICANT: THOMPSON, Craig
APPLICANT: MOORE, Jeffrey
APPLICANT: BUUDMAN, Ed T.
                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Corresponds to SEQ ID NO:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-12
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-12-06
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                                                                                                                                                                                                                DATABASE ACCESSION NUMBER: Human DATABASE ENTRY DATE: 1997-06-25 RELEVANT RESIDUES: (1)..(1023)
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                              FEATURE:
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177 LGNGIQTMSASVQRAVAMSSGDVPGA---RGAVEGILIQQVFESGG----
                                                                              126 PRLPTKRKASEEARAAAPAAL-----TPRGT--ASPGSQLKAKPPKKPESSAEQQRLP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 ECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSC
                                          45 PRTP-----EVRAAAAGALGNHVVSGSPAGAAGAGPAAPAEGAPGAAPEPPPAGRARP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BUURMAN, Ed T.
BRADLEY, John
DESILVA, Thamara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZHU, Shuhao
LONG, Fan
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KOMARNITSKY, Svetlana
MENDILLO, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOORE, Daniel
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                                                                                                                                                                                                                                                           Genbank/CAA72189
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                                                                                                                                                           DB 9;
                                                                                                                       163;
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US-09-764-864-1184
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                                                                                                                                                                 US-09-764-864-1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1184 LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1184, Application US/09764864 Patent No. US20020132753A1
                                                                                     Matches
                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE LOCATION: (40) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (31)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (35)
                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                LOCATION: (44)
OTHER INFORMATION:
                                                                                                                                                                                                    LOCATION: (102)
                                                                                                                                                                                                                           NAME/KEY: SITE
                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
101 RXKKPDSPPKVLEPENKQEKTEKEEEKTNVGRTLRRSPR----ISRPTAKVAEIRDQKA 155
                                    111 KGRKPPAVPKALVPPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 AAPPAAQTLAASGPA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 DGTDVLRCTHCAAAFHWRCHFPAGTS-RPGTGLRCRSCSGDVTPAPVEGVLAPSPARL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 RPPGHP-AG------PPTAAP-----AVPPPAAAQNGGSAGAAPAPAPAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 FVGAAAPPAPAAPS-----PAPATLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 HLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGEEVR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 LLNSHHAAAPAVSLVNNGPAALLPLPKPAAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 PEPAPAGPAKPAGPAALAARAGPGPGP-------GPGPGPGPGKPAGPGAAQTINGSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 GEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSV----- 279
                                                                              Local Similarity les 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APGPAKDDTASHEPALHRDDLESLLSEHTFDGILQWAIQSMARPAAPFP 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGPQRPGPPSPRRPLVPAGPAPPAAKLRPPPEG-----SAGACAPVPAAAAVAAG 149
                                                                              5.4%;
ilarity 22.3%;
Conservative 39
                                                                                                                                                                                                                                              Xaa
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                                                                                                                                                                                                                                                                                                            Xaa
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                                                                                                                                                                                Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                              equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -PAGVSGQPGPGA-----AAAAPAPGVKAESPKRVVQ 350
                                                                                   39;
                                                                              Score 156; DB 1
Pred. No. 0.019;
9; Mismatches 1
                                                                                                                                                                                                                                                                                                        any of the naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                               of the naturally occurring
                                                                                                                     DB 10;
                                                                                100;
                                                                                                                       Length 432;
                                                                                Indels
                                                                                88;
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                                                                              Gaps
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US-10-189-971-20

: Sequence 20, Application US/10189971

: Publication No. US20030028907A1
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SEQ ID NO 7
LENGTH: 1400
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NOTEBORN, Mathleu Hubertus Maria
APPLICANT: DANEN-VAN OORSCHOT, Astrid Adriana Anna
APPLICANT: ROHN, Jennifer Leigh
APPLICANT: WEISS, Bertram
TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
FILE REFERENCE: 4725US
CURRENT FILING DATE: US/09/764,176
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Description of Sequence: Amino acid
OTHER INFORMATION: leic acid sequence of AAP-
                                                                                                                                                                                                                                                                                                  280 PAPLALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 QRLPLGNG---IQTMSASYQRA-----VAMSSGDYPGARGAVEGILIQQVFESG-----G 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          703 KKPDSPPKVLEPENKQEKTEKEEEKTNVGRTLRRSPR-----ISRPTAKVAEIRDQKADK 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 RKPPAVPKALVPPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQ 172
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                                                                                                                                                               CQHKLLCEKLEEQLQDLDVALKKKERAERRKERLVYVGISIENIIPPQEP 946
                                                                                                                                                                                                             C------PQEP
                                                                                                                                                                                                                                                                                                                                                     SR----TRGRWKYSSNDESEGSGSEKSSAASEEEEEKESE-----EAILADDDEP
                                                                                                                                                                                                                                                                                                                                                                                                SKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KR---GEGEDEVEEESTALQKTDKKEILKKSEKDTNSK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVPAPLALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.3%; Score 155; DB 10;
22.4%; Pred. No. 0.078;
ative 38; Mismatches 99,
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US-09-819-104A-5
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; ORGANISM: homo
US-10-189-971-20
                                                                                         GENERAL INFORMATION:
APPLICANT: Chep, J. Don
TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
TITLE OF INVENTION: AND USES THEREFOR
TITLE OF INVENTION: AND USES THEREFOR
CURRENT APPLICATION NUMBER: US/09/819,104A
CURRENT EILING DATE: 2001-03-779
CURRENT FILING DATE: 2001-03-779
                                                                                                                                                                                                                                                                     Sequence 5, Application US/09819104A
Publication No. US20030027137A1
SEQ ID NO 5
                                         PRIOR APPLICATION NUMBER: 60/193,138 PRIOR FILING DATE: 2000-03-29 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                   SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: TUVENTION: No. US20030028907A1el Human Kielin-like Proteins and Polynucl.
TITLE OF INVENTION: Same
FILE REFERENCE: LEX-0360-USA
CURRENT APPLICATION UMBER: 2002-07-03
CURRENT EILING DATE: 2002-07-03
CURRENT EILING DATE: 2002-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/302,949
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/315,634
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 AGTSRPGTGLRCRSCSG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ALVPPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 -ARLARSPVRSRSAQSPPVPCLPLAASSAQGACCPSCDSCTYHSQVYANG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 SLCPARQCP----ADTQARSLGSAALSAMAVSTRDTSIRARRPSDSKSGASVSAAP----
                                                                                                                                                                                                                                                                                                                                                                                                                    A-----RGDCCPDCDG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQGPCCPSCDGCLYQGKEFASGERFPSPTAACHLCLCWEGSVSCEPKACAPAL---CPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCPQCPAAPAPAGCPRPGAAHARHQEYFSPPGDPCRRCLCLDGSVSCQRLPCPPAPCAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -RPQEP----PVETPLPPGLRSAGEEVRGPPGEPLAG---MDTTLVYKHLPAPPS--AAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCPNDCSGCAFGGKEYPSGADFPHPSDPCRLCRCLSGNVQCLARRCVPLPCPEPVLLPGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFYTPSKFEDSGSGKNKARSSSG------PKPLVRAKGAQG-AAPGGGEARLGQQG
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22.7%;
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Pred. No. 0.088;
14; Mismatches 164; Indels 13
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US-09-764-176-7

ORGANISM: Homo sapiens FEATURE:

Matches Query Match

65;

Conservative

Local

Similarity

RESULT 7 US-09-764-176-7

GENERAL INFORMATION:

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RESULT 8

GENERAL

INFORMATION

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RESULT 10
US-09-925-301-844

Sequence 844, Application US/09925301

Patent NO. US20020052308A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Pro
FILE REFERENCE: PA106
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                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 844
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
                                                       NAME/KEY: SITE LOCATION: (36)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
TYPE: PR
                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                   NAME/KEY: SITE
LOCATION: (64)
                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1117 ---GVLERQ-----LGAISQGMSVQLRVPHSEHA-----KPMGPLTMELPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1078 SYTPPGHPLPLGLHDSARPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1018 RGKSRSPVPPAEKEAEKPAFFPAFPTEGQSYRLSPHAGHRLPSHPPREVIKTSTRADPLF 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          477 GDVTPAPVEGVLAPSPARLAPGPAKDDTASHEPALHRDDLESLLSEHT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 LCVGPEGQQNLAPGARCGVCGDGTDV-LRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      973 PPIVTKVHEPP-----REDTVP-PKPVPPVPPPTQHLQPEGDVSQQSG-----GSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 DVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       796 ASGPPSPEPSPSPAAPPATVDKDEQEAPAAPAPQTEDAKEQKSEAEEIDVGKPEEPEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 AS-PGSQLKAKPPKKPESSA--EQQRLPLGNGIQTMSASVQRAVA------MSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      746 ESVPSPRSEATKDTGPKPTGTEALPAATQPPVPPPEEP-----AAAPAEPSPVPD 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 DSFPKDVDLSQPRKGRKP-----PAVPKALVPPPRLPTKRKASEEARAAAPAALTPRGT 151
  INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSDSSATCSADEVDEPEGGDKGRLLSPRPSLLTPAGDPRASTSPQKPLDLKQLKQRAAAI 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEPPVET-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2462
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                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids, Proteins
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equals
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Pred. No. 0.23;
any of the naturally occurring L-amino acids
                                                          any of the naturally occurring
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US-09-764-176-3
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                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: NOTEBORN, Mathieu Hubertus Maria
APPLICANT: DANEN-VAN OORSCHOT, Astrid Adriana
                                                                                                                                                                                                                                                Sequence 3, Application US/09764176 Patent No. US20020127553A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 121;
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                                                                              APPLICANT: ROHN, Jennifer Leigh
APPLICANT: WEISS, Bertram
TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
FILE REFERENCE: 4725US
                                        CURRENT APPLICATION NUMBER: US/09/764,176
CURRENT FILING DATE: 2001-01-17
SOFTWARE: PatentIn version 3.0
                     NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
LOCATION: (358)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 GIQTMSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKKCIQVGGEFYTP---SKF 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 -----ASEEARAAAPAAL-----TPRGTA--SP-GSQLKAKPPKKPESSAEQQRLPLGN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 AEEPRPQEP-----PVETPLPPG-----LRSAGEEVRGP-----PGEP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 RVNSGLSSDPHFXEPGPMVRGVGGTPRDSAGVSPFPPKRRERPPRKPELLQEESLPP--- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 RLDQVIHSNPAGIQQALAQLSXRQXSVTAPGGHPRHKPGPPQAPQG--PSPRPPTRYEPQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 RLQPILDSFPKDVD--LSQ------PRKGRKPPAVPKALVPPPRLPTKRK-- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        ----PSLHPYRSQPLYLPPGPA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                   DVTPAPVEGVLAPSPARLAPGPA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTATSRKSYRPSSMEPWMEPLSPFEDVAGTEMSQSDSGVDLSGDSQVSSGPCSQRSSP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPE----GQQNLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEPPRRPPPAPHDGDRKELPREQPLPPGPIGTERSQXTDRGTE-PGPIRPSHRPGPPVQF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PEPSSSGQRLYPEVFYGSAGPSSSQI----SGGAMDSQLHPNSGGFRPGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPR 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (103)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LAGMDTTLVYKHLPAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -DGGLKGAAEG------PPKR--PGG----SSPLNAVPCEGPPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 149; DB 1
Pred. No. 0.073;
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CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILLYG DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-01-27
PRIOR FILING DATE: 1997-06-03
                                                                                        US-09-976-740-43
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LENGTH: 538
               Matches 106;
                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/09976740 Publication No. US20020194633A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                           NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                             TYPE: PRT
                                                                                                        ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature OTHER INFORMATION: Description of Sequence: amino acid sequence of the analyzed OTHER INFORMATION: on of the Apoptin-associating clone AAP-2-II
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                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 SR----TRGRWKYSSNDESEGSGSEKSSAASEEEEEKESE------EAILADDDEP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 ORLPLGNG---IQTMSASVQRA-----VAMSSGDVPGARGAVEGILIQQVFESG-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 RKPPAVPKALVPPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 SKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 KR----GEGEDEVEEESTALQKTDKKEILKKSEKDTNSK------VSKVKPKGKVRWTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 KKPDSPPKVLEPENKQEKTEKEEEKTNVGRTLRRSPR----ISRPTAKVAEIRDQKADK 208
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       5.1%; Score 147.5; Diarity 22.6%; Pred. No. 0.08; Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%; Score 148.5; DB 23.2%; Pred. No. 0.049;
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ILLCDSCDSGYHTACLRPPLMIIPDGEWFCPP 347
                                       DB 9;
     136;
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                                       Length 538;
 Indels 181;
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Best Local Sim Matches 106;

Similarity

5.1%;

Score 147.5; [ Pred. No. 0.08;

DB 12; Length 538;

Indels 181; Gaps

Conservative

47; Mismatches 136;

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APPLICANT: AIJONA, ANIBAL A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: ATHEROSCLEROSIS

FILE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/023,529

CURRENT FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930
US-10-023-529-43
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                                                  PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 43
LENGTH: 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43, Application US/10023529
Patent No. US20020129388A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lees, Ann M.
              ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 WRCSSCLQATVQEVQPRAEE-PRPQEPPVETPLPPGLRSAGEEVRGP-PGE-----PLA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 QQGSVPAPLALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 ------RIERTRLG--ALALPRGDRP-GRAPPAASARPSRSKRGGEERVL 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 PPQPQPPPEGGAVRAGGAA--RPVSLREVVRYLGGSGGAGGRUIRGRVQGLLEEEAAARG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------AQHHQLNGERGPQSAKERVKEWTPCGPHQGQDEGRGPAPGSGTRQVFSMA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lees,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robert S.
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Query Match  5.1%; Score 147.5; DB 12; Length 538; Best Local Similarity 22.6%; Pred. No. 0.08; Matches 106; Conservative 47; Mismatches 136; Indels 181; Gaps 26;  Qy 56 POAFHALLSWLITQDSTAILDFWRVLFK-DYNLERYGRLOPILDSFPKDVDLSQPRKGRK 114   :	FILING DATE: 1996-11-27 APPLICATION NUMBER: US 60/048, FILING DATE: 1997-06-03 R OF SEQ ID NOS: 53 RO 43 NO 43 TH: 538 : PRT NISM: Homo sapiens 3-523-43	APPLICANT: Lees, Ann m.  APPLICANT: Lees, Robert S.  APPLICANT: Law, Simon W.  APPLICANT: Low, Simon W.  APPLICANT: Arjona, Anibal A.  APPLICANT: Arjona, Anibal A.  APPLICANT: Arjona, Anibal A.  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  TITLE OF INVENTION: ATHEROSCLEROSIS  FILE REFERENCE: 10797-004001  CURRENT APPLICATION NUMBER: US/10/023,523  CURRENT APPLICATION NUMBER: US/09/616,289  PRIOR APPLICATION NUMBER: US/09/616,289  PRIOR APPLICATION NUMBER: US/09/517,849  PRIOR APPLICATION NUMBER: US/09/517,849	LACTOR ACTION OF THE PROPERTY	Db 228 PPQPQPPPEGGAVRAGGAARPVSLREEVVRYLGGSGAGGRLTRGRVQGLLEEEAAARG 285  Qy 219 GSKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLG 274  Qy 219 GSKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLG 274  Db 286	SYKGSISYRNAARVQP VPPPRLPTKRKASEEA-RAAAP
220 SKKCIQVGGEFYTPSKFEDSSSGKNKARSSSG	Query Match  5.0%; Score 145.5; DB 9; Length 1251; Best Local Similarity 21.7%; Pred. No. 0.26; Matches 97; Conservative 44; Mismatches 166; Indels 139; Gaps 21;  Qy 121 ALVPPPRIPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQORLPLGNG 180	TITLE OF INVENTION: No. US20030028907Alei Human Kielin-like Proteins and Polynucli TITLE OF INVENTION: Same  FILE REFERENCE: LEX-0360-USA CURRENT APPLICATION NUMBER: US/10/189,971 CURRENT FILING DATE: 2002-07-03 PRIOR APPLICATION NUMBER: US 60/302,949 PRIOR FILING DATE: 2001-07-03 PRIOR FILING DATE: 2001-07-03 PRIOR FILING DATE: 2001-08-29 NUMBER OF SEQ ID NOS: 25 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 16 LENGTH: 1251 TYPE: PRT ORGANISM: homo sapiens US-10-189-971-16	387 GMDTILVYKHLPAPPSAAPLPGLDSSALHPLLCYGPEGQQ 426 11	219 GSKKCLQVGGEFYTPSKFEDSGSKNKAKSSGFPLVKRKGAQGAPG	

Db	ργ	Дb	Qy	D	δĀ	D	, Q
386 ALCPFPARGDCCPDCDG 402	452 AFHWRCHEPAGTSRPGTGLRCRSCSG 477	326 CPPAPCAHPROGPCCPSCDGCLYQGKEFASGERFPSPTAACHLCLCWEGSVSCEPKACAP 385	399 APPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAA 451	266 PEPVILIPGECCPOCPAAPAPAGCPRPGAAHARHQEYFSPPGDPCRRCLCLDGSVSCQRLP 325	353 EEPRPQEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLP 398	206 PCAHPLPGTCCPNDCSGCAFGGKEYPSGADFPHPSDPCRLCRCLSGNVQCLARRCVPLPC 265	321 ACLSPPLREIPSGTWRCSSCLQATVQEVQPRA 352

Search completed: March 13, 2003, 17:58:32 Job time : 23 secs

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Title:
Perfect score:
Sequence:
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Maximum
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2: /cgn2_6/ptodata/2;
3: /cgn2_6/ptodata/2;
4: /cgn2_6/ptodata/2;
5: /cgn2_6/ptodata/2;
6: /cgn2_6/ptodata/2;
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Maximum Match 100%
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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PCT-US-106418-1
US-08-942-686-2
US-08-942-686-2
US-09-579-181-1
US-08-976-255-11
US-08-976-255-11
US-08-976-255-11
US-08-976-255-11
US-08-976-255-11
US-08-98-47-9B-6
US-08-98-47-9B-6
US-09-370-838-216
US-09-370-838-216
US-09-370-838-216
US-09-370-838-216
US-09-562-737-38
US-09-562-737-38
US-08-545-860D-28
PCT-US94-04496-28
US-08-9559-26
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US-08-959-26-255-73
US-09-562-737-33
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479 VTPAPVEGVL-----APSPARL-APGPAKDDTASHEPALHRDDLESLLSEHTFDGILQW 531

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US-09-249-181A-2

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Sequence 1, Application PC/TUS9106418
GENERAL INFORMATION:
APPLICANT: Oklahoma Medical Research, Foundation, et al
TITLE OF INVENTION: Antigens Associated with Polymyositis
TITLE OF INVENTION: and with Dermatomyositis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Seelig, Hans Peter
APPLICANT: Renz, Manfred
TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
FILE REFERENCE: 8484-0059-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09249181A Patent No. 6440679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 CVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGD 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 EPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 SVSDGSTSRSSRSRKKLRTTK------KKKKGEE-EVTAVDGYETD------HQDY 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 SGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 -RRKPKGSPRVPDAKKPKPKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSY 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 QRAVAMSSGDVPGARGAVEGILIQQVFESGG----SKKCIQVGGEFYTPSKFED----- 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 PFKGSSGASVAAAAAAAVAVVESMYTATEV-APPPPPVEVPIRKAKTKEGKGPNA----- 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 PTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQTMSASV 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQ 358
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                       Sequence 2, Application US/08942686 Patent No. 6183988 GENERAL INFORMATION:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
      APPLICANT:
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                                                                                                                                                                                                                                                      240 VPPPRPLQGRSEREFFVK---WVGLSYW 264
                                                                                                                                                                                                                                                                                                                   504 TASHEPALHRDDLESLLSEHTFDGILQW 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                454 HWRCHFPAGTSRPGTGLRCRSCSGDVTPAPVEGVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 ү----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 YKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAAAF 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KWSCPHCEKEGYQWEAKEEEEEEYEEE-----GEE-EGEKEEE----DDHME 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 GQQGSVPAPLALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSG
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 TWRCSSCLQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 GGSKKCIQVGGEFYTPSKFE---DSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEAR-L 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watch 8.1%; Score 236.5; DB 5; Length 351;
Local Similarity 25.6%; Pred. No. 1e-11;
nes 84; Conservative 28; Mismatches 131; Indels 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GGKRKKGGSSDEGPEPEAEESDLDSGSVHSASGRPDGP---VRTKKLKRGRPGRKKKKVL
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AMINO ACID
Bloch, Donald B.
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-249-181A-2

SEQ ID NO 2

LENGTH:

1912

Matches Query Match

Local Similarity 23.1 nes 97; Conservative

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373 299

RESULT 3 PCT-US91-06418-1

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

ADDRESSEE:

E: Kilpatrick & Cody 100 Peachtree Street

STATE: CITY: STREET:

Georgia

Atlanta

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/027,347
FILING DATE: 02-OCT-1996
CLASSIFICATION: 514
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: LEUKOCYTE-SPECIFIC PROTEIN AND GENE, AND TITLE OF INVENTION: METHODS OF USE THEREOF NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                               399
                                                                                                                                                                                                                                                                      137
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                                                                                                                                                                                                                                                                                                                                                                                                                                   105
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                                                                                                                                                                                                                                                                                                        219 VSCKLAIQIDEGESEEMPKLLPYDTEETFDLKTPQVTNEGEPEKGLCLLPGEGEEGSDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 LLTQDSTAILDFWRVLFKDYNLERYGRLQPILDSF------PKDV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 REFRENKVEIASAITRPFPFLMGLRDRSFISEQMYEHFQEA--FRNLVPVTRVMYCVLSE 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 RLLRLHRTEIAVAVDSAFPLLHALADHDVVPE---DKFQETLHLKEKEGCPQAFHALLSW 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                         RRQKNSQQNDNSKADGQVVSSEKKANVNLKDLSKIRGRKRGKPGTRFTQSDRAAQKRVRS 458
                                                                                                                                         KCSCVMCFSEEVPGSPEARTESDQACGTMDTVDIANNSTLGKPKRKKRKKRGHGWSRMRM 398
                                                                                                                                                                                                                        SEMCDGEERQEASSSLARRGSVSSELENHPMNEEGESEELASSLLYDNVPGAEQSAYENE 338
                                                                                                                                                                                                                                                                                                                                                                                       PYGKQENSNACHEMDDIAVPQEALSSSARCEPGFSSESCEQLALPKAGGGDAEDAPSLLP 218
                                                                                                     QTMSASVQRAVAMSSGDV-----
                                                                                                                                                                                                                                                                -----EARAAAPAALTPRGTAS----- 160
                                                                                                                                                                                                                                                                                                                                                136
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202-371-2540
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------GAVEGILIQQVFESGGSKKCIQV-GGEFYTPSKFEDSG 240
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ER: 0609.4330001/JAG/BJD
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SEQ ID NO 4
LENGTH: 1593
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 08/323,460
EARLIER FILING DATE: 1994-10-14
EARLIER APPLICATION NUMBER: 08/049,254
EARLIER FILING DATE: 1993-05-15
EARLIER APPLICATION NUMBER: 08/410,602
EARLIER FILING DATE: 1995-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/628,829A CURRENT FILING DATE: 1996-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Johnson, Gary L.
TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To Exter
FILE REFERENCE: CPI-004DVCP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 08/472,934
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1995-05-15
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                                                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                                                                                                 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154
                          391 TLVYKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 PRKGRKPPAVPKALVPPPRLPTKRKASEEARAAA------PAALTPRGTAS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624 SPGSQQCCQESEVLERQMCPEE 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   459 RASRKHKDETVDFKAPLLPVTCGGVKGILHKKKLQQGILVKCIQTEDGKWFTPTEFEIKG 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
                                                                           IREKLKATCMPAWKHEWLERRNRRGPVVVKPIP--IKGDGSEVNNLAAEPQGEGQAG---
                                                                                                                                                                                                                                  DECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPR 356
                                                                                                                                                                                                                                                                                     RRPAHLLPVAGARGRGCRSESLPARAGPPPPGAASRCGSHSA----
                                                                                                                                                                                                                                                                                                                                        -----PLVRAKG-----AQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                            I------LIQQ------VFESGGSKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPK 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PPPSPAGTSECSPREKMAAAAGDRASSSGFPGAAAASPEAGGGGGGGGALQG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGSQLKAKPPKKPESSAE----QQRLPLGNGIQTMSASVQRAVAMS---SGDVPGARGAVEG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTCAARPPAAPRS-----RAPAGRRGPARARARALGSSARPPTRPPLRPPPALSP----- 85
                                                                                                                                                                                    -ELAAARDSG-----ARSPAGAEPPSAAAPSGREMENKETLKGLHKMEDRPEERM 279
                                                                                                                                                                                                                                                                                                                                                                                              SGAPAAGAAGLLREPGSAGPSARTGGGGTCAKCGVWSWTSCR-----SSRSSSPPP 188
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                                                                                                                                 -----PPVETPLPPGLRSAGEEVRG----PPGEPLAGMDT 390
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Indels 200;
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; ORGANISM: Human
US-09-579-181-2
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US-09-579-181-2
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Best Local Similarity
Matches 114; Conserv
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SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chrivia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 16153-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
CURRENT FILING DATE: 2000-05-25
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                                                                  1371 PVMAPSSTPGTSL----ASASPVPAPTP-VLAPSSTQTMLPAPVPSPLPSPASTQTLALA 1425
           1426 PAL---
                                                                                                                                                                                                                                                                                            1214 ---LTSVTPPLAPVVPAAPGPPSLQPSGASPSASALTLGLATAPSLSSSQTPGHPLLLAP 1270
                                                                                                                                                                                                                    1271 TSSHVPGLNSTVAPACSPVLVPASALASPFPSAPNPAPAQASLLAPASSASQALATPLAP 1330
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                                 509 PALHRDDLESLLSEHTFDGILQWAIQSM--ARPAAPFPS 545
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                                                                                                         HFPAGTSRPGTGLRCRSCSGDYTPAPVEGVLAPS-----PARL---APGPAKDDTASHE 508
                                                                                                                                                MAAPQTAILAPSPAPPLAPLPVLAP----SPGAAPVLASSQTPV----
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-APTLGGSSPSQTLSLGTGNPQGPFPT 1454
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22.0%; Pred. No. 0.001;
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                                                                                                                                                                                                                                                                                                                             -----PSGTWRCSSCLQATVQEVQPRAEEPRPQEPPVETP 365
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US-09-051-019-2
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                                                                                                         Sequence 2, Application US/09051019
Patent No. 6103229
GENERAL INFORMATION:
APPLICANT: KAHMANN, Regine and
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Best Local Similarity
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Patent No. 6365372
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
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TITLE OF INVENTION: SNE2 Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 16153-4247
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-27
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CURRENT FILING DATE: 2000-05-25
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                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                               1477 MAAPQTAILAPSPAPPLAPLPVLAP-----SPGAAPVLASSQTPV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 KDVDLSQPRKGRKPPAV------PK-ALVP-PPRLPTKRKASEEARAAAPAA 145
                                                                                                                                                                                                                                                          PAL----APTLGGSSPSQTLSLGTGNPQGPFPT 1600
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                                                                                                     KAHMANN,
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                                                                          Regulatory gene from Ustilago maydis
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jono, Keith E.
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2289 amino aci
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect version 6.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 AAGAAEALANATPVLETPTQSPSTVASTRRSARKRSEATSTPASSSRNSLQLTSTPMTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 -QQGRKRVSVPVIDG--RSVDLYQLKLVISSLGGYDAVCRARKWSDATRKIGYSDKESGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 LLNSLS-ADARASQNYQEQL------QKFHA-----
                                                                                                                                       COUNTRY:
                                                                                                                                                                                                              STREET: 633 West F:
STREET: Suite 4700
CITY: Los Angeles
                                                                                                             ZIP:
                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage COMPUTER: IBM AT-compatible, Pentium processor OPERATING SYSTEM: Windows 98 COUNTRIBED: GOLDMAN 10 FOR THE PROCESSION FOR THE PROCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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FILING DATE: 31-MAR-1998
                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPTKRKAS-----EEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGN 179
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                                                                                                                                                                             Los Angeles
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633 West Fifth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
storage
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US-08-545-860D-55
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                                                                                                                                                                Patent No. 6040140 GENERAL INFORMATION:
                                                                                                                                                                                 Sequence 55, Application US/08545860D Patent No. 6040140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER.

FILING TO DOS 5.0

LUCIWARE: FASTSEQ for Windows 2.0

CURRENT APPLICATION DATA:

FILING TO DOS 5.0
                                                         APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        1124 SSEFQGPPGLLSGPAPQKRMGGPGT-----PRAPLRLALPGLPAA 1163
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LENGTH: 1384 amino aci
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FILING DATE: No. 6136581ember 22,
ATTORNEY/AGENT INFORMATION:
                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 GDRAPGPELGLPS---TGQPSEQVC--LRPGVSGEAQGSGPGEVL--------
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                                                                                                                                                                                                                                                                                                                                               375 -EEVRGPPG-----EPLAGMDTTLVYKHLPAPPSAAPLPGLDSS 412
                                                                                                                                                                                                                                                                                                                                                                                                                              325 PPLREIPSGTWRCSSCLQATVQEVQPRAEEP---RPQEPP-----VETPLPPGLRSAG- 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 V----AMSSGDVPGAR--GAVEGILIQQVFESGGSKKCIQVG--GEFYTPSKF--EDSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        847 AIKLASALNGSSSSPEVEAPSSEDEDTAEATSGIFTDTSSDGLQARRPDVVPAFRSLQKQ 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         790 PK---LATEAEGTTGPRLPLPSVPSPSQEGAPLPSEEASAPDAPDALPDSPTPATGGEVS 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (213)
TELEX: 67-3510
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    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                       PPLLQLEGSSPEPSTCPSGLVPE-PPEPQGPAKVRPGPSPSCSQFFLLTPVP--LRSEGN 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCEPQAFAELASEGEGPGPETRLSTSLSGLNEKNPYRDSAYFSDLEAEAEATSGPEKKCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 5.1%; Score 149; DB 4; Similarity 23.6%; Pred. No. 0.00097;
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Woodcock, Washburn, Kurtz, Mackiewitz
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1093 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                 Best Local Sir
Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/320,559
ETILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/062,443
ETILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/971,094
ETILING DATE: 30-OCT-1992
PRIOR APPLICATION NUMBER: US 07/888,839
PRIOR APPLICATION NUMBER: US 07/888,839
PRIOR APPLICATION NUMBER: US 07/888,839
PRIOR APPLICATION NUMBER: US 07/805,093
ETILING DATE: 27-MAY-1992
PRIOR APPLICATION NUMBER: US 07/805,093
ETILING DATE: 11-DEC-1991
ATTORNEX/AGENT INFORMATION:
NAME: DELUCA ESG., MAIK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1262
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE NCHYPOTHETICAL: NC
107 SQP-------RGRKPPAVPKALVPPPRLPTKRKASEEARAAAPAALTP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US92/10930
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                    169 DNVKYCGYCKYHFSKMKTSRHSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGFISGRRSRSASPSTQQE 228
                                                                                                                                                                    111 VPHDRFNKTCYICEETGRESKAASGACMTCNRHGCRQAFHVTCAQMAGLLCEEE--VLEV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                78 WRVLFKDYNLERYGRLQPILDS----------
                                                                                                                                                                                              FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: No. 6040140ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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N FOR SEQ ID NO:	; INFO	
TELEFAX: (215) 568-3439		
OMMUNICATION INFORMATION:	; TE	
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CLASSIFICATION:		
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ARRITATION DAT		
SOFTWARE: PatentIn Release #		
SYSTEM: PC-DOS/MS-DO	٠.	
IBM PC	٠.	
TYPE: Fl	٠. :	
COMPUTER READABLE FORM:	`	
CUNTRY		
STATE: Pennsylvania		
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OF SEQUENCES: 86		
OF INVENTION: Resulting from Chromosome Abnormalities in th		
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457 CHFPAGTSRPGTGLRCRSCSGDVTPAPVEGVLAPSPARLAPGPAK 501	Qy .	
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; MOLECULE TYPE:
; HYPOTHETICAL: 1
; ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08396479B Patent No. 5612455 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                         STATE: California Cali
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Pred. No. 0.001;
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RESULT 13
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Sequence 6, Application US/08818823 Patent No. 5708158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-8700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/396,479B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 902 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                  427 NLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAP 483
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                                                                                                                                                                                                          376
                                                                                                                                                                                                                                        313 GPFDYVG-APPAESIPQKTRRTSS-EQAV---ALPRSEEP----ASCNGKLPLG----AE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                     PLVRAK------GAQGAAPGG-----
                                                                                                    QLE---
                                                                                                                                                                                                        EVRGPPG---EPLAGMDTTLVYKHLPAPP--SAAPLPG----LDSSALHPLLCVGPEGQQ 426
                                                                                                                                                                                                                                                                           RAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGE 375
                                                                                                                                                                                                                                                                                                             TPSSASPALSRRGSLGEEGSEPPPPPPLPLARDP-----GSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKC-IQVGGEFYTPSK-----FEDSG-----SGKNKARSSSG---PK 253
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                                                                                                                                                                      ESVAPPGGSRKEVAGMD----YLAVPSPLAWSKARIGGHSPIFRTSALPPLDWPLPSQYE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REAGAQGGGAFFSPSPGSSSSSSSSFFSDASDEAALYAACDEVESELNEAASRFGLGSPL
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                                                                                                    ---LRIEVQPRAHH-RAHYETEGSR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SPRDYPPPEG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                   -----GEAR-----
                                                                                                    -GAVKAAP 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----FGGY 155
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GENERAL INFORMATION:
APPLICANT: HOEY, Timothy

TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS
ADDRESSEE: FLEHR, HO

CITY: San Francisco

California

STREET:

4 Embarcadero Center, Suite 3400

HOHBACH, TEST, ALBRITTON & HERBERT

STATE: COUNTRY:

USA

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RESULT 14
US-09-370-838-216
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          GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-818-823-6
                                                                Sequence 216, Application Patent No. 6444425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
APPLICANT: Mohamath,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 494-8771
TELEX: 210 277299
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 02-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OSMMAN, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
                                                                                                                                                           416 QLE------LRIEVQPRAHH-RAHYETEGSR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                        427 NLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAP 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 RPPPPRPGMHSPPPR-PAPSPGTWESQPARSVRLGGPGGGAGGAGGAFVLECPSIRITSI 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01
FILING DATE: 14-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                           ESVAPPGGSRKEVAGMD----YLAVPSPLAWSKARIGGHSPIFRTSALPPLDWPLPSQYE
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                                                                                                                                                                                                                                                                                                                           RAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGE 375
                                                                                                                                                                                                                                                                                                                                                                                            PSPRASPRPWTPEDPWSLYGPSPGGRGPEDSWLLLSAPGPTPASPRPASPCGKRRYSSSG
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                                                                              US/09370838
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RESULT 15
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 216
                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sin
Matches 126;
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TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR US
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
PARLIER FILING DATE: 1999-04-02
                                                                                                             TITLE OF INVENTION: NOVEL HUMAN INSULINOMA-ASSOCIATED CDNA NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                              APPLICANT: Lan, Michael S.
APPLICANT: No. 6225049kins, Abner L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 527
                                                                                                                                                                                                                                                                                                                                                                 444 PEGDTDPSTPPAPPTPP-----HPATPGDGFPS--NDSGFGGSFEWA 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446 CTHCAAAFHWR--CHFPAGTSRPGTG-----LRCRSCSGDVT--------PAP 483
                                  ADDRESSEE: Knobbe, Martens, Olson
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: California
COUNTRY: U
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                               384 SADADAARPLRGLLKSPRGADEPEDSELERKRKMVSFHGDVTVYLFDQETPTNELSVQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 SEQIKARLSRLSLALPPLTLTPFPGPGPRRPPWEGADAGAAGGEAGG-----AG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 AQGAAPGGG-----EARLGQQGSV-----PAPLALPSD------PQLHQKNE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 GAV--EGILIQQVFESGGSKKCIQVGGEFYTPSKFE-DSGSGKNKARSSSGPKPLVRAKG 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQEVQPRAEEPRPQEPPVE-TPLP-PGLR------SAGEEVRGPPGEPLAGMDTTL 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DECAVCRDGGE-LICCDG------CPRAFHLACLSPPLREIPSGTWRCSSCLQAT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGTAPGGGPGSGVDAKAGWVDNTRPQPPPPPLPPPPEAQPRRLEPAPPRARPEVAPEGE
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Pred. No. 0.00085;
                                                                                                Olson & Bear
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Search completed: March 13, 2003, 17:54:53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 510 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: NIH012.012A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: ISTACLSON, Ned A.
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/901,715
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,489
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                                                                                                                                     463 TSRPGTGLRCRSCSGDVTPAPVEG---VLAPSPARLA 496
                                                                                                                                                                                                                             424 --GQQNLAPGAR---CGVCGD-------GTDVLRCTHCAAAFHWRCHFPAG 462
                                                                                                                                                                                                                                                                             372
                                                                                                                                                                                                                                                                                                                                                                     313 -HRRWHKPRPAPAAARAPEPEAAARAEAREAPGGGSDRDTPSPGGVSESGSEDGLYECHH 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 RGRAGGAARPLGEFI-CQLCKEEYADPFALAQHKCSRIVRVEYRCPECAKVFSCPANLAS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 GKRPPPPTAAEPPAKAVKAPGAKKPKAI---RKLH--FEDEVTTSPVLGLKIKEGPVEAP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 GAQGAAPGGGE--ARLGQQGSVPAPLALPSDPQLHQKNEDEC---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 LIQQVFESGGSKKCIQVGGE--FYTPSKFEDSGSGKNKARSSSGPKP-----LVRAK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 KP-----PKKPESSAEQQR------LPLGNGIQTMSASVQRAVAMSSGDVPGARGAVEGI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 HPAPLYSPTRPVSREHEKHKYFERSFNLGSPVSAESFPTPAAL-LGGGGGGGGASGA---- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 4.9%; Score 142.5; DB 4; Length 510; Local Similarity 22.8%; Pred. No. 0.00089;
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                                                                                       -SSPGLTRHINKCH-----PSENRQVILLQVPVRPA 509
                                                                                                                                                                                   GAGVLGLSASAECHLCPVCGESFASKGAQERHLRLLHAAQVFPCKYCPATFY-----
                                                                                                                                                                                                                                                                           CAKKFRRQAYLRKHLLAHHQALQAKGAPLAPPAEDLLALYP----GPDEKAPQEAAGDGE 427
                                                                                                                                                                                                                                                                                                                                                                                                                   VQPRAEEPRPQEPPVETPLP-PGLRSAGEEVRG-----PPGEPLAGMDTTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AVCRDGGELICCDGCPRAF--HLACLSPPLREIPSGTWRCSSCLQ-----ATVQE 347
                                                                                                                                                                                                                                                                                                                       -----VYKHLPAPPSA-----APL--PGLDSSALHPLLCVGPE-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GGGGTC---GGDPLLFAPAELKMGTAFSAGAEAARGPGPGPPLPPAAALRPP 198
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OM protein - protein search, using sw model
Run on:
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Title: Perfect score: Sequence: US-09-509-595B-2
2902
1 MATDAALRRLLRLHRTEIAV......DGILQWAIQSMARPAAPFPS 545 March 13, 2003, 17:50:47; Search time 14 Seconds (without alignments) 1614.614 Million cell updates/sec

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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75 mus mus		P54258 rattus norv	Q14934 homo sapien		Parded outpar	homo	n6 homo		Q9wv48 rattus norv	P47156 saccharomyc							nome	Light	homo ci				009698 schizosacch		homo sapie	٠, ١	7	9 droso	homo	Domo	9 homo	3 homo	z0e3 mus m	043918 homo sapien	Description		

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BRF1_HUMAN	HRX_MOUSE	TCOF_HUMAN	SMCY_MOUSE	BAT2_HUMAN	SMCY_HUMAN	ICPO_HSV11	IA1_HUMAN	SMCX_MOUSE	Y211_HUMAN	REQC_CHICK	SMCX_HUMAN
P55201 homo sapien	P55200 mus musculu	Q13428 homo sapien	Q62240 mus musculu	P48634 homo sapien	Q9by66 homo sapien	P08393 herpes simp	Q01101 homo sapien	P41230 mus musculu	Q92610 homo sapien	· P58270 gallus gall	P41229 homo sapien

## ALIGNMENTS

in the

cytoplasm in

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GLU-83; CYS-85; C
VARIANT ARG-278.
PubMed-11524731;
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Kumar P.G., Larry

Kao K.-J., She J.-X.;

"The autoimmune regulator (AIRE) is "The autoimmune regulator" (AIRE) is "The autoimmune regu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scott H.S., Heino M., Peterson P., Mittaz L., Lalioti M.D., Betterle C., Cohen A., Seri M., Lerone M., Romeo G., Collin P., Salo M., Metcalfe R., Weetman A., Papasavvas M.-P., Rossier C., Nagamine K., Kudoh J., Shimizu N., Krohn K.J.E., Antonarakis S.E., "Common mutations in autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy patients of different origins."; Mol. Endocrinol. 12:1112-1119(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heino M., Peterson P., Kudoh J., Shimizu N., Antonarakis S.E Scott H.S., Krohn K.J.E.; "APECED mutations in the autoimmune regulator (AIRE) gene."; Hum. Mutat. 18:205-211(2001).
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Heino M., Scott H.S., Chen Q., Peterson P., Maeenpaeae U.,
Papasavvas M.-P., Mittaz L., Barras C., Rossier C., Chrousos
Stratakis C.A., Nagamine K., Kudoh J., Shimizu N., Maclaren
Antonarakis S.E., Krohn K.J.E.;
Mutation analyses of North American APS-1 patients.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS APECED LEU-15; MET-16; GLU-83; CYS-85; CYS-90; ARG-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98381937; PubMed-9717837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hum. Mutat. 13:69-74(1999).
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domain.";
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LEU-28; CYS-302 AND CYS-437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pitkaenen J., Vaehaemurto P., Kro
"Subcellular localization of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bjorses P., Pelto-Huikko Ulmanen I.;
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                                  nuclear receptors.

DOMAIN: The HSR domain is required for localization on tubular structures (N-terminal part) and for homodimerization.

DOMAIN: Disruption of the first PHD domain has been shown to 10
                                                                                                                                                      splicing.

TISSUE SPECIFICITY: Widely expressed. Expressed at higher level thymus (medullary epithelial cells and monocyte-dendritic cells) pancreas, adrenal cortex, and testis. Expressed at lower level i the spleen, fetal liver and lymph nodes. Isoforms 2 and 3 seem the test irequently expressed than isoform 1, if at all DOMAIN: The L-X-Z-L-L repeats may be implicated in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Probable transcriptional regulator protein that binds DNA as dimer and tetramer, but not as a monomer. Binds to G-doublets in an A/T-rich environment; the preferred motiv is a tandem repeat of ATTGGTTA combined with a TTATTA-box. May be involved in immune regulation.

SUBUNIT: Homodimer and homotetramer. Interacts with CREBBP.

SUBCELLULAR LOCATION: Nuclear and cytoplasmic; associated with the combined with a succession of the combined with the com
                                                                                                                                                                                                                                                                                                                                                                                                   tubular structures and in discrete nuclear dots ressembling ND10 nuclear bodies. May shuttle between nucleus and cytoplasm. ALTERNATIVE PRODUCTS: At least 3 isoforms; 1/AIRE-1 (shown here). 2/AIRE-2 and 3/AIRE-3; may be produced by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 276:19597-19602(2001).
             transcriptional
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the autoimmune regulator protein.
argeting and transcriptional activation
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domain has been shown
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-: DISEASE: Defects in AIRE are a cause of autoimmune poly-
endocrinopathy candidiasis ectodermal dystrophy (APECED), also
called autoimmune polyglandular syndrome type I (APS-I), an
autosomal recessive disease characterized by: (1) autoimmune
polyendocrinopathies: hypoparathyroidism, adrenocortical failure,
polyendocrinopathies: hypoparathyroidism, pernicious anemia, and
hepatitis; (2) chronic mucocutaneous candidiasis; (3) ectodermal
dystrophies: vitiligo, alopecia, keratopathy, dystrophy of dental
enamel, nails and tympanic membranes. In addition, a high
proportion of patients develop squamous cell carcinoma of the oral
mucosa. The disease is reported worldwide but is exceptionally
the Iranian jews (incidence 1:9000).
-: SIMILARITY: CONTAINS 1 HSR DOMAIN.
-: DATABASE: NAME-AARE; NOTE-ARTICLE on AIRE and APECED;
WWW-"http://chr21.rz-berlin.mpg.de/APECED.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligomerization.
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on could trigger
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

Pfam; PF00628; PHD; 2. Pfam; PF01342; SAND; 1. Pfam; PF03172; Sp100; 1. SMART; SM00249; PHD; 2. SMART; SM00258; SAND; 1. PROSITE; PS50864; SAND; 1.
PROSITE; PS50864; SZP\_PHD\_1; 2.
PROSITE; PS50016; ZZP\_PHD\_2; 1.
Nuclear protein; DNA-binding; Transcr
Repeat; Phosphorylation; Alternative Disease mutation.
DOMAIN 1 InterPro; InterPro; InterPro; AB006682; BAA23988.1; -. AB006683; BAA23989.1; -. AB006684; BAA23990.1; -. AB006684; BAA23991.1; -. AB006684; BAA23992.1; -. AB006685; BAA23992.1; -. AB006685; BAA23993.1; -. AB006685; BAA23985; B 240300; AJ009610; HGNC:360; AIRE. IPR000770; IPR004865; IPR001965; 63 414 516 1 BAA95560.1; CAA08759.1; 106 280 343 475 133 520 11 67 418 520 292 Sp100. Znf\_PHD. SAND\_domain. PHD-TYPE 1.
PHD-TYPE 2.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
4 X 5 AA REPEATS OF L-X-X-L-L. Transcription regulation; Zinc-finger; splicing; Polymorphism;

MATDAALRRLLRLHRTEIAVAVDSAFPLLHALADHDVVPED KROETLHLKEKEGCPOAFHALLSWLLTODSTAILDFWRVLF KDYNLERYGRLQPILDSFPKOPULSOPRKGREPAVPKAIV PPPRLPTKRKASEEARAAPAALTPRGTASPGSOLKAKPPK KPESSAEQORLPLONGIOTMSASVQRAVAMSSGDVPGARGA VEGILIQQVFESGGSKKCIQVGGEFYTDSKFEDSGSGKNKA RSSSGFKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPS DPQLH -> MWLVYSSGAPGTQQPARNRVFFPIGMAPGGVC

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RESULT 2
AIRE_MOUSE
ID AIRE_M
AC 0920E3
AC 09JUM7
DT 15-JUN
DT 15-JUN
DT 15-JUN
DT AUTOIM
DE AUTOIM
DE AUTOIM
DE AUTOIM
DE ECTODE
GN MUS MUU
OC EUKARY
OC MAMMAI
OX NCBI_T
RN [1]
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                                                      Shi J.-D., Wang C.-Y., Marron M.P., Rua Detter J.C., She J.-X.; "Chromosomal localization and complete autoimmune regulator gene (Aire)."; Autoimmunity 31:47-53(1999).
                                                                                                                                                                                                                                            AIRE_MOUSE STANDARD; PRT; 552 AA.

920E3; 09JLX0; 09JLW1; 09JLW2; 09JLW3; 09JLW4; 09JLW5; 09JLW6;

09JLW7; 09JLW8; 09JLW9; 09JLW0;

15-JUN-2002 (Rel. 41, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 41, Last annotation update)

Autoimmune regulator (Autoimmune polyendocrinopathy candidiasis ectodermal dystrophy protein homolog) (APECED protein homolog).
MEDLINE=99160890; PubMed=10049735
                 STRAIN=129
                             SEQUENCE FROM N.A.
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID-10090;
                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1A). PubMed=10593569;
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"The autoimmune regulator (AIRE) is a DNA-binding protein.";
J. Biol. Chem. 276:41357-41364(2001).

-i-FUNCTION: Probable transcriptional regulator protein that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11533054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT STRUCTURE, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kolmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halonen M., Pelto-Huikko M., Eskelin P., Peltonen L., Ulmanen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney, a
PubMed=11156688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Expression and alternative splicing gene (Aire).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10550218;
Ruan Q.-G., Wang C.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blechschmidt K., Schweiger M., wertz R., France M.-L.;
Christensen H.-M., Rosenthal A., Lehrach H., Yaspo M.-L.;
"The mouse Aire gene: comparative genomic sequencing, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mittaz L., Rossier C., Heino M., Petersen P., Krohn K.J.E., Gos A., Morris M.A., Kudoh J., Shimizu N., Antonarakis S.E., Scott H.S.; "Isolation and characterization of the mouse Aire gene."; Biochem. Biophys. Res. Commun. 255:483-490(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10022980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3C AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AIRE) gene responsible for autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99168902; PubMed=10049587;
                                                                                                           TISSUE SPECIFICITY: Expression may be restricted to a small number of scattered cells in most tissues. Highly expressed in a few cells in the medulla of the thymus. Detected at very low levels in thymus, lymph node, liver, brain, ovary, lung, testis, kidney, heart, spleen, bone marrow, skeletal muscle and adrenal gland. Isoforms 3a to 1d predominate, isoforms 2a to 2d are intermediate and isoforms 3a to 3d are expressed at extremely low levels.

DOMAIN: The L-x-x-L-L repeats may be implicated in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA as dimer and tetramer, but not as a monomer. Binds to G-doublets in an A/T-rich environment; the preferred motiv is a tandem repeat of ATTGGTTA combined with a TTATTA-box. May be involved in immune regulation (By similarity).

SUBCULULAR LOCATION: Predominantly nuclear but also cytoplasmic. SUBCLULUAR LOCATION: Predominantly nuclear but also cytoplasmic. Found in nuclear body-like structures and in a filamentous vimentin-like pattern.

ALTERNATIVE PRODUCTS: At least 12 isoforms; la (shown here), 1b, 1c, 1d, 2a, 2b, 2c, 2d, 3a, 3b, 3c and 3d; are produced by alternative colinion to the structure of the struc
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nuclear receptors.

DOMAIN: The N-terminal HSR domain is required on tubular structures (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1c, 1d, 2a, 2b, 2c, 2d, 3a, 3b, 3d alternative splicing. Isoforms 3a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         nonfunctional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55:322-326(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laloraya M., Wang C.-Y., Ruan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.A. (ISOFORM 1A), AND SUBCELLULAR LOCATION and Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOD, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        She
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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to 3d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are probably
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                                         for localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2B;
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Matches
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Best Local
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InterPro; IPR0004865; Sp100.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001965; Znf_PHD; 1.
InterPro; IPR001965; Znf_PHD; 1.
InterPro; IPR001965; Znf_PHD; 2.
INTERPRO; SM00258; SAND; 1.
INTERPRO; INTERPRO; Znf_PHD; 2.
INTERPRO; INTERPRO; Znf_PHD; 2.
INTERPRO; INTERPRO; Znf_PHD; 2.
INTERPRO; IPR001964; Znf_PHD; 2.
INTERPRO; IPR001964; Znf_PHD; 2.
INTERPRO; IPR001965; Znf_PHD; 2.
INTERPRO; IPR001965; Znf_PHD; 2.
INTERPRO; IPR001965; Znf_PHD; 2.
INTERPRO; IPR001965; Znf_PHD.
InterPro; IPR001966; Znf_PHD.
Inter
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DOMAIN
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                                                                                                                                                                                                                                                       VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ243821; C, MGD; MGI:1338803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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the European Bioinformatics Institute. They
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L; AF105002; AAD46421.1; AF128772; AAF36482.1; AF128773; AAF36482.1; AJ007715; CAAO7620.1; AV079556; AAD20444.1; AV132243; CAB36909.1; AF128115; AAF36460.1; AF128115; AAF36461.1; AF128116; AAF36464.1; AF128119; AAF36464.1; AF128119; AAF36464.1; AF128112; AAF36466.1; AF128121; AAF36466.1; AF128121; AAF36466.1; AF128122; AAF36466.1; AF128124; AAF36466.1; AF128124; AAF36466.1; AF128124; AAF36469.1; AF128124; AAF36469.1; AF128125; AAF36469.1; AF128124; AAF36469.1; AF128125; AAF3649.1; AF128125; AAF128125; A
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                                                                                    69.1%; Score 2005; 71.8%; Pred. No. 4
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                                                                                                                                                                                      WW;
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                                                                                                                                                                                                      MISSING (IN ISOFORM 1C, ISOFORM 1D,
ISOFORM 2C, ISOFORM 2D, ISOFORM 3C AND
ISOFORM 3D).

MISSING (IN ISOFORM 1B, ISOFORM 1D,
ISOFORM 2B, ISOFORM 3B AND ISOFORM 3D).

MISSING (IN ISOFORM 2A, ISOFORM 2B,
ISOFORM 2C AND ISOFORM 2D).
ISOFORM 2C AND ISOFORM 2D,
ISOFORM 2C AND ISOFORM 2D,
ISOFORM 3C AND ISOFORM 3D,
ISOFORM 3C AND ISOFORM 3B,
ISOFORM 3C AND ISOFORM 3D,
ISOFORM 3C AND ISOFORM 3D).
                                                          37;
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PHD-TYPE ZINC FINGERS.
SAND DOMAIN.
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SAND.
PHD-TYPE 1.
PHD-TYPE 2.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
4 X 5 AA REPEATS OF L-X-X-L-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; Zinc-finger;
                                                                                                                                                                               ISSING (IN ISOFORM 3A, ISO SOFORM 3C AND ISOFORM 3D). BF30F8F66B71239A CRC64;
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing
                                                                                    4e-103;
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-!- FUNCTION: POSSIBLE TRANSCRIPTION ACTIVATOR (BY SIMILARITY)!- SUBUNIT: Central component of the nucleosome remodelling and histone deacetylase (NuRD) complex.	ACE OF 121-654 FROM N.A. "Thymus; tE=96013633; PubMed=7560064; Nilasena D.S., O'Brien C.A. ular analysis of a major ant ular analysis of a major ant colored the major and	SEQUENCE FROM N.A.  TISSUE-Fetal; MEDLINE-97470991; PubMed=9326634; MEDLINE-97470991; PubMed=9326634; MOOdage T., Basrai M.A., Baxevanis A.D., Hieter P., Collins F.S.; "Characterization of the CHD family of proteins."; Proc. Natl. Acad. Sci. U.S.A. 94:11472-11477(1997). [2]	sapiens ( yota; Met lia; Euth TaxID=96(	15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Chromodomain helicase-DNA-binding protein 3 (CHD-3) (Mi-2 autoantigen 240 kDa protein) (Mi2-alpha).	ULT 3 3_HUMAN CHD3_HUMAN STANDARD; PRT; 1944 AA. Q12873;	543 PLAETPPESS 552	AAPFPS 545	483 P-VEGVLAP-SPARLAPGPAKDDTASHEPALHRDDLESLLSEHTPDGILQMAIQSMAR 538	23 EGRPGPAPSARCSVCGDGTEVLRCAHCAAA	GARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVT	363 ETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCVGP 422 	303 ROGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEPPV 362	45 KNKARSGSSLKPVVRAKGAQVTIPGRDEQKVGQQCGVPPLPSLPSEPQVNQKNEDE	BARLGQQGSVPAP	184 MSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKKCIQVGGEFYTPSKFED-SGSG 242  :      ::	.25 LPPRPPTKRKAL	PRIPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQRLPLGNGIQT 1	 AGPKAAV 1	WLLTQDSTAILDFWRVLFKDYNLERYGRLQPILDSFPKDVDLSQPRKGRKPPAVPKALV 1	5 DGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKFQETLRLKEKEGCPQAFHALL 64

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SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00249; PHD; 2.
SMART; SM00184; RING; 2.
                                                                                                                                                                                                                                                                                                 Zinc-finger
                                                                                                                                                                                                                                                                                                                      Chromatin regulator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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SERA OF DERMATOMYOSITIS
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DISEASE: ONE OF THE MAIN ANTIGENS REACTING WITH ANTI-MI-2 POSITIVE
                                 KLR---
                                                                                      PAVPKALVPPPRL-----PTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSA 170
                                               EQQRLPLGNGIQTMSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKKCIQVGGEF
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PS50016; ZF_PHD_2;
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PS50013; CHROMO_2; 2.
PS00690; DEAH_ATP_HELICASE;
PS01359; ZF_PHD_1; 2.
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IPR001841;
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Helicase_C.
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Pred. No. 1.
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POLY-LYS.
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InterPro; InterPro; InterPro; InterPro; InterPro; InterPro;

IPR001410; IPR002464; IPR001650; IPR000330; IPR001965;

DEAD.

DEAH\_box.

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SNF2\_N.

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IPR000953;

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15-JUL-1999
15-JUN-2002
                                                                                                                                       MIM; 603277
                                                                                                                                                                       EMBL; X86691;
                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chromodomain helicase-DNA-binding protein 4 (CHD-4) (Mi-2 autoantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seelig H.P., Moosbrugger I., Ehrfeld H., Fink T., Ren
"The major dermatomyositis specific Mi-2 autoantigen
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear. DISEASE: ONE OF THE MAIN ANTIGENS REACTING WITH ANTI-MI-2 POSITIVE SERA OF DERMATOMYOSITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: POSSIBLE TRANSCRIPTION ACTIVATOR (BY SIMILARITY). SUBUNIT: Central component of the nucleosome remodelling an histone deacetylase (NuRD) complex.
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Metazoa; Chordata; C
Metazoa; Primates; C
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Catarrhini; Hominidae;
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RESULT 5
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ID SP11_HUMAN ST
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Pfam; PF00628; PHD; 2.
SMART; SM00298; CHROMO; 2.
SMART; SM00497; DEXDC; 1.
SMART; SM00490; HELLCC; 1.
SMART; SM00184; RING; 2.
SMART; SM00184; RING; 2.
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ZN_FING
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                                                           ALKGKVQKILIWKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVK---WQGMSYW
                                                                      VTPAPVEGVL-----APSPARL-APGPAKDDTASHEPALHRDDLESLLSEHTFDGILQW
                                                                                                                CVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGD
                                                                                                                                                                               EPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALHPLL
                                                                                                                                                                     CEVCQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEK---EGIQWEAKED---
                                                                                                                                                                                                         SVSDGSTSRSSRSRKKLRTTK-----KKKKGEE-EVTAVDGYETD-----HQDY
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PF00385;
PF00628;
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2; PS50013; CHROMO_2; 2.
2; PS00690; DEAH_ATP_HELICASE; 1
2; PS00590; DEAH_ATP_HELICASE; 1
2; PS01359; ZF_PHD_1; 2.
2; PS50016; ZF_PHD_2; 2.
2; PS50016; ZF_PHD_3; ATP-
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                 STANDARD;
         Q9HCT8;
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         Q14976; Q14977;
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POLY-GLU.
POLY-GLU.
POLY-ASP.
POLY-ALA.
POLY-PRO.
POLY-LYS.
POLY-LEU.
POLY-GLU.
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PHD-TYPE
CHROMO 1.
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                  PRT;
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ches 172;
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MIM;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on in the European Bioinformatics Institute as long as its content is in no ware by non-profit institutions as long as its content is in no ware.
                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nuclear hormone receptor transcriptional coactivator Mol. Cell. Biol. 20:6138-6146(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bloch D.B., Nakajima A., Gulick T., Cnicne J. J., Ozen, de La Monte S.M., Bloch K.D.;
"Spill localizes to the PML-Spi00 nuclear body and may "Policy of the PML-Spi00 nuclear body and may "PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and may be provided in the PML-Spi00 nuclear body and m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spli0 nuclear body protein (Speckled 110 kDa) (
coactivator Spli0) (Interferon-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Spleen;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kadereit S., Gewert D.R., Galabru J., Hovanessian "Molecular cloning of two new interferon-induced,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94043285; PubMed=7693701;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kidney and pancreas.
INDUCTION: By interferon gamma and by all-tr PTM: Phosphorylated (1soform 2).
SIMILARITY: CONTAINS 1 BROMODMAIN.
SIMILARITY: CONTAINS 1 HSR DOMAIN.
SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
SIMILARITY: CONTAINS 1 SAND DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 268:24432-24441(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate, testis, ovary, small in levels in heart, brain, placenta,
                                                                                                                                                                                     w; HGNC:5401;
604457; -.
                                                                                                                                                                                                                            AF280094; AAF99318.1; -. AF280095; AAG09826.1; -. BC019059; AAH19059.1; -.
                                                                                                                                                                                                                                                                           L22343; AAD13402.1
AF280094; AAF99318
                                                                                                                                                                                                                                                                                                  122342; AAA18806.1; -.
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                                                                                          IPR001487; Bromodomain.
IPR000770; SAND_domain.
IPR004865; Sp100.
IPR001965; Znf_PHD.
                           SAND; 1
Sp100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung, liver,
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PROSITE; PS50016; Z
PROSITE; PS00633; E
PROSITE; PS50014; E
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QVFESGGSKKCIQ-VGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEA
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                    KCARKSRSKEKKKEKDICSSSKRRFQKNIHRRGKPKSDTVDFHCSKLPVTCGEAKGILYK
                                                            MNEGKRSQKTPSTPRRVTQGAASPGHGIQEKLQVVDKVTQRKDDSTWNSEVMMRVQKART
                                                                                                                         PRGTASP--GSQLKAK-----PPKKPESSA---
                                                                                                                                              PQEMPHSPLGSMPEIRDNSPEPNDPEEPQEVSSTPSDKKGKKRKRCIWSTPKRRHKKKSL
                                                                                                                                                                                      DPVLPLPALIQEGRSTSVTNDKLTSKMNAEEDSEEMPSLLTSTVQVASDNLIPQIRDKED
                                                                                                                                                                                                                               PILLEAPTGLAEGSSLHTPLALPHHKPPQPSCSPCAPRVSEPGTSSQQSTEILSESPSPS
                                                                                                                                                                                                                                                                                             PQAFHALLSWLLTQDSTAILDFWRVLFKDYNLERYGRLQPILDSFPKDVDLSQPRKGR--
                                                                                                   PRGTASSRHGIQKKLKRVDQVPQKKDDSTCNSTVETRAQKARTECARKSRSEEIIDGTSE
                                                                                                                                                                                                                                                                         SRVVHNILTQL---ERTFULSLLVTLFSQINLREYPULVTIYRSF-KRVGASYERQSRDT
                                                                                                                                                                                                                                                                                                                  AMEEALFQHFMHQKLGIAYAIHKPFPFFEGLLDNSIITKRMYMESL----
                                                                                                                                                                                                                                                                                                                                                           al Similarity
119; Conser
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SM00258;
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SAND; 1.

4; SAND; 1.

6; ZF_PHD_2; 1.

3; BROMODOMAIN_1; FALSE_NEG.

13; BROMODOMAIN_2; FALSE_NEG.

14; DNA-binding; Trans-acting factor; Zinc-finger;

15; Bromodomain; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
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                                                                                                                                                                                                                                                                                                                                                                                                   78504 MW;
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                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN ISOFORM 3).

MISSING (IN ISOFORM 4 AND
IRDYGE -> NVSSSS (IN ISOF
MISSING (IN ISOFORM 2).

T -> D (IN REF. 3).

T -> M (IN REF. 1; AAA188
                                                                                                                                                                                                            TKRKASEEARAAAPAALT - -
                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                  -GNGIQ--
                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKNSDECEV -> SGLCSVLQE (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAS -> AL (IN ISOFORM 5).

RKNSDECEVCCQGGQLLCC -> SGLLLCPPRINLKRELNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN ISOFORM 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKAPHGRERKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHK -> PPQ (IN ISOFORM 5).
IRDNSPEPNDPEEPQEVSSTPSDK -> MASSGVKNTPRWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN ISOFORM MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BROMODOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHD-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                           Mismatches
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M (IN REF.
S (IN REF.
                                                                                                                                                                                                                                                                                                                                                                   228;
                                                                                                                                                                                                                                                                                                                                                                  NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN ISOFORM 4 AND ISOFORM 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVSSSS (IN ISOFORM 2).
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.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IN ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                           138;
                                        VAMSSGDVPGARGAVEGILIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECEPTOR INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                      l; AAA18806).
l; AAA18806).
                                                                                                                                                                                                                                                                                                                                                                             Length 689;
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                 TMSASVQRA--
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ID TFIA_H
AC 015164
DT 15-JUL
DT 16-CCT
DT 16-CCT
DT 16-CCT
DE Transc
GN HOMO S
CC Eukary
OC MAMMAT
ON NCBLI
RP SEQUEN
RC TISSUE
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RT Transc
RI J. Bio
RX MEDLIN
RA VENTLI
RA KOKEN
RA VENTLI
RA COCOGE
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015164; 095854;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequal control of the control o
                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-:- SIMILARITY: CONTAINS 2 BOX-TYPE ZINC FINGERS.
-:- SIMILARITY: CONTAINS 1 BROWODOWAIN.
-:- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1999) to the SWISS-PROT data bank.
-!- FUNCTION: INTERACTS SELECTIVELY IN VITRO WITH THE AF2-ACTIVATING DOMAIN OF THE ESTROGEN RECEPTORS, ASSOCIATION WITH DNA-BOUND ESTROGEN RECEPTORS REQUIRES THE PRESENCE OF ESTRADIOL.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De The H.; "TIF1gamma, a novel member of the transcriptional intermediary 1 family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thenot S., Henriquet C., Rochefort H., "Differential interaction of nuclear re transcriptional coactivator hTIF1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription intermediary TIF1A OR TIF1.
                                                                                                                                                             EMBL; AF009353; AAB63585.1;
EMBL; AF119042; AAD17258.1;
HSSP; P29590; 1BOR.
                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cavailles V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncogene 18:1209-1217(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (SHORT ISOFORM).

MEDLINE-99144725; PubMed-10022127;
Venturini L., You J., Stadler M., Galien R., Le
Koken M.H.M., Mattei M.-G., Ganser A., Chambon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                        TRANSFAC; T04945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 477-510 (LONG ISOFORM).
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MEDLINE=97277352; PubMed=9115274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLGE-
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Primates;
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annotation update)
factor 1-alpha (TIF1-alpha).
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on P., Loss
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00502; BBC; 1.
SMART; SM00336; BBCX; 2.
SMART; SM00297; BROMO; 1.
SMART; SM00249; PHD; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
CONFLICT
CONFLICT
873 LSKPEVEYDCDAP 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                   171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                     131 KRKASEEARAAADAALTPRGTASPG-----SQLKAKPPKK------PESSA
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat.
                                                                                                                                                                                                                                        631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01406; BBOXZNFINGER. PRINTS; PR00503; BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pranscription
                                                                                                                                                                                                                                                   71 STAILDEWRYLEKDYNLERYGRLQPILDSFPKDVDLSQPRKGRKPPAVPKALVPPPRLPT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001841;
                       ATVQEVQPRAEEP 355
                                                         LALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQ
                                      --KEDDP-----NEDWCAYCQNGGELLCCEKCPKVFHLSCHVPTLTNFPSGEWICTFCRD
                                                                                                         CIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAP
                                                                                                                                                       EQORLPLGNGIQTMSASVQRAVAMSS-----GDVPGARGAVEGILIQQVFESGGSKK 222
                                                                                                                                                                                --ASSVGSRGSSGSSSKPAGADSTHKVPVVMLEPIRIKQENSGPPENYDFPVVIVKQESD
                                                                                                                                 EESRPQNANYPRSILTSLLLNSSQSSTSEETVLRSDAPDSTGDQPGL--------
                                                                                                                                                                                                                            STIMLD--NIVRKDINID-HGQPRPPSNRTVQSPNSSVPSPGLAGPVTMTSVHPPIRSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pro; IPR001841; znf_ring.
PF00097; zf-C3HC4; 1.
PF00439; bromodomain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E; PS00633; BROMODOMAIN_1; FALSE_NEG.
E; PS50014; BROMODOMAIN_2; 1.
E; PS50019; ZF_BBOX; 2.
E; PS01359; ZF_BBD_1; 1.
E; PS50016; ZF_HD_2; 1.
E; PS50016; ZF_RING_1; 1.
E; PS50089; ZF_RING_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00628; PHD; 1.
PF00643; zf-B_box; 2.
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001487;
IPR000315;
IPR001965;
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulation;
                                                                                        -HQDNSSNGKSEWLDPSQKSPL---
                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                             24.6%;
                                                                                                                                                                                                                                                                                                     7.88;
                                                                                                                                                                                                                                                                                                                                 116831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Znf_Bbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bromodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing; Nuclear protein; Coiled coil;
                                                                                                                                                                                                                                                                                                                               PHD-TYPE.

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

BROMODOMAIN.

MISSING (IN SHORT ISOFORM).

AASAAAS -> RLGCAP (IN REF. 1).

SAAPS -> RGG (IN REF. 1).

SAAPS -> ARRSA (IN REF. 1).

SAPS -> ARRSA (IN REF. 1).

O -> N (IN REF. 1).

A -> T (IN REF. 1).

M -> R (IN REF. 1).

M -> R (IN REF. 1).

M -> R (IN REF. 1).
                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repressor; DNA-binding; Bromodomain;
                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                             Score 227; DB 1;
Pred. No. 1.4e-05;
6; Mismatches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COILED COIL (POTENTIAL).
POLY-GLN.
NUCLEAR RECEPTOR BINDING SITE (NRBS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOX-TYPE 1.
BOX-TYPE 2.
                                                                                                                                                                                                                                                                                                                           D341E8022AACC67E CRC64;
                                                                                                                                                                                                                                                                            104; Indels
                                                                                                                                                                                                                                                                                                  Length 1050;
                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                           Gaps
                                                                                   819
                                                                                                                                                                                                                              687
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RX MEDLINE-20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Gorayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.+L.C., Blazed R.G., Champe M., Feiffer B.D.,
RA Ballew R.M., Basu A., Barel R.G., Champe M., Feiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borits K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
RA Borits R.D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dukov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Moshrefi N., Skupski M.P., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Manger E., Shen H., Weissenbach J.,
RA Wang S.-Y., Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
CHDM_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHDM_DROME STANDARD; PRT; 1982 AA.
097159; 09VW50;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Chromodomain helicase-DNA-binding protein Mi-2 homolog (dM1-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kehle J., Beuchle D., Treuheit S., Christen B., Kennison J.A., Bienz M., Muller J.; "dMi-2, a hunchback-interacting protein that functions in Polycomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99055400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                        FUNCTION: VITAL ROLE IN DEVELOPMENT. PROTE HUNCHBACK (HB) PROTEIN THAT IS CRITICAL FC COMPLEX (BXC) GENES. MAY ALSO FUNCTION IN REPRESSION OF HOX GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282:1897-1900(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pubmed=9836641;
                                                                                     PMENT. PROTEIN BINDS TO A PORTION CRITICAL FOR REPRESSION OF BITHOR FUNCTION IN POLYCOMB GROUP (PCG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS OF GLY-737
                                                                                                              ITHORAX
                                                                                                                                  Q
```

-!- SUBCELLULAR LOCATION: Nuclear
-!- SIMILARITY: BELONGS TO THE SNI
-!- SIMILARITY: CONTAINS 2 CHROMO

SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY SIMILARITY: CONTAINS 2 CHROMO DOMAINS. SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.

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                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00385; chromo; 1.
Pfam; PF00628; PHD; 2.
SMART; SM00298; CHROMO; 2.
SMART; SM00487; DEXDC; 1.
SMART; SM00480; HELICC; 1.
SMART; SM00249; PHD; 2.
SMART; SM00184; RING; 2.
                                                                                                                                                                                                                                                        CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                   NP_BIND
SITE
                                                                                                                                                                                                                                                                               MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF119716; AAD17276.1; -.
EMBL; AE003515; AAF49099.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CAUTION:
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
   336
                          357
                                                                                            220
                                                                                                                   304
                                                                                                                                                               260
                                                                                                                                                                                  110 RKGRKPPAVPKALVPPPRLPT-----KRKASEEARAAPAALTPRGTASPGSQLK- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [nterPro;
                                                                                                                                        160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene model prediction
RCSSCLQATVQEVQPRAEEPRPQEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYK 395
                      KNKLKKTKNFPEGEDGEHEHQDYCEVCQQGGEIILCDTCPRAYHLVCLEPELDEPPEGKW
                                                                                                                                                              KKGRRPSG------KVPTLKIKLLGKRKRDSSDEEQDAS
                                             QGSVPAPLALPSDPQLHQKNEDECAVCRDGGELICCDGCPRAFHLACLSPPLREIPSGTW 335
                                                                                        SKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLG---
                                                                                                                ERMLQKSDDSADEKEAPVS-----SKADNSAPAA-
                                                                                                                                     AKPPKKPESSAEQQRLPLGNGIQTMSASVQRAVAMSSGDVPGARGAVEGILIQQVFESGG
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; IPR001410; DEAD.
; IPR002464; DEAH_box.
; IPR001650; Helicase_C.
; IPR001330; SNF2_N.
; IPR001965; Znf_PHD.
; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FBgn0013591; Mi-2
                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000953; Chromo.
                                                                                                                                                                                                                                                                               239
1279
1672
737
                                                                                                                                                                                                                                                          1982
                                                                                                                                                                                                                                                                                                                                                 437
488
612
755
875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76; SNF2_N; 1.
71; helicase_C; 1.
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ref.2 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                    regulation;
                                                                                                                                                                                                                                                        Å,
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZF_PHD_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHROMO_1; FALSE_NEG.
                                                                                                                                                                                                                                                                              762
878
16
76
248
1287
1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEAH_ATP_HELICASE; 1.
ZF_PHD_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMO_2;
                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                     7.8%;
20.2%;
                                                                                                                                                                                                                                                        224199 MW;
                                                                     -QDDGSG------APVVRKK-----AKTKIGNKFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                Helicase; Nuclear protein; Repeat;
                                                                                                                                                                                                            39;
                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                   POLY-GLU.
POLY-GLU.
POLY-GLU.
                                                                                                                                                                                                                                                      G->D: IN ALLELE MI-2-5; LARVAL LETHAL.
G -> A (IN REF. 1).
MW; ED8E256D1AD0AC2F CRC64;
                                                                                                                                                                                                                                                                                                                                                  DEAH
                                                                                                                                                                                                                                                                                                                                                                                                PHD-TYPE 1.
PHD-TYPE 2.
                                                                                                                                                                                                                                                                                        POLY-ASP
                                                                                                                                                                                                                                                                                                                                                                          CHROMO 2
                                                                                                                                                                                                                                                                                                                                                                                    CHROMO
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                    227;
2.
                                                                                                                                                                                                                                                                                                                                                   вох.
                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions
                                                                                                                                                                                                         DB 1; 1
2.7e-05;
hes 93;
                                                                                                                                                                                                                               Length 1982
                                                                                                                                                                                                         Indels 172;
                                                                                                                                                             -GASERDSDLEF 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                         Gaps
                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            commercial
                        416
                                                                                                                                      219
                                                                                                                332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on
                                                                                                                                                                                                          11;
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RESULT 8

TFIA_MOUSE
ID TFIA_M
AC Q64127
DT 15-JUL
DT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 몽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFIA_MOUSE STANDARD (06127; 064126; 15-JUL-1999 (Rel. 38, 015-JUL-1999 (Rel. 38, 015-JUL-2002 (Rel. 41, 015-JUN-2002 (Rel. 41, 015-JUN-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            le Douarin B., Zechel C., Garnier J.-M., Lutz Y., Tora L., Pierra Heery D., Gronemeyer H., Chambon P., Losson R.; "The N-terminal part of TIF1, a putative mediator of the ligand-dependent activation function (AF-2) of nuclear receptors, is fus B-raf in the oncogenic protein T18."; EMBO J. 14:2020-2033(1995).
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S78221; AAB34290.1; -. EMBL; S78219; AAB34289.1; -. HSSP; P29590; 1BOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 2 B BOX-TYPE ZINC FINGERS.
-!- SIMILARITY: CONTAINS 1 BROWODOMAIN.
-!- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription intermediary factor 1-alpha (TIF1-alpha).
                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                          TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                               TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIF1A OR TIF1
                                                                                                                   InterPro;
                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95262642; PubMed=7744009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 FCLNPPLDTIPDGDWRCPRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396
                                                                          ANSFAC; T02215; Tifla. D; MGI-109275; Tifla. CterPro; IPR003649; Bbox.C. terPro; IPR001487; Bromodomain. terPro; IPR0019315; Znf_Bbox. terPro; IPR001965; Znf_HD. terPro; IPR001965; Znf_HD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Nuclear:
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: DETECTED IN ALL ADULT TISSUES, WITH THE
HIGHEST EXPRESSION LEVEL IN TESTIS.
DISEASE: PARTICIPATES IN A CHROMOSOMAL TRANSLOCATION THAT PRODUCES
A TIFLA-BRAF (T18) ONCOGENE ORIGINALLY ISOLATED FROM A FURFURAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: INTERACTS SELECTIVELY IN VITRO WITH THE AF2-ACTIVATING DOMAIN OF THE ESTROGEN RECEPTORS. ASSOCIATION WITH DNA-BOUND ESTROGEN RECEPTORS REQUIRES THE PRESENCE OF ESTRADIOL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCHFPAGTSRPGTGLRCRSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCPHC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCAAAFHW
                                             PF00097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEPATOMA.
                                         2f-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EADGGAAEEEDDDEHQEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CRVCKDGGELLCCDSCPSAYHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            γď
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pierrat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fused
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455
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```

PF00628;

PHD;

Zinc-finger; Alternative splicing;

Repeat;

Proto-

oncogene;

```
D3_CABLE

CHD3_CABEL

CHD3_CAEEL

C Q22516; Q18794;

T 15-JUL-1999 (Rel. 38, Created)

T 15-JUL-1999 (Rel. 38, Last sequence update)

JT 15-JUL-1999 (Rel. 41, Last annotation update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

Thromodomain helicase-DNA-binding protein 3 home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DR Pfam, PF00643; zf-B_box; 2.

PFAMTS; PR01406; BBOXZNFINGER.

PRINTS; PR01406; BBOXZNFINGER.

PRINTS; PR00503; BRCMNDDOMAIN.

PROMART; SM00502; BBC; 1.

PROMART; SM0036; BBOX; 2.

PROMART; SM00249; PHD; 1.

PROSITE; PS00634; PROMODOMAIN_1; FALSE_NEG.

PROSITE; PS0014; PROMODOMAIN_2; 1.

PROSITE; PS00119; ZF_BBOX; 2.

PROSITE; PS00119; ZF_PHD_1; 1.

PROSITE; PS0015; ZF_PHD_1; 1.

PROSITE; PS00016; ZF_PHD_2; 1.

PROSITE; PS00016; ZF_RING_1; 1.

PROSITE; PS0009; ZF_RING_2; 1.

PROSITE; PS0009; ZF_RING_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 STAILDEWRVLEKDYNLERYGRLQPILDSFPKDVDLSQ----PRKGRKPPAVPKALVPPP 126
                                                                                                                                                                                                                                                                                                                                                                                      VHVGETRKEDDPNEDWCAVCQNGGELLCCEKCPKVFHLTCHVPTLTNFPSGEWICTFCRD
                                                                                                                                                                                                                                                                                                                                                                                                                NYPRSILTSLLLNSSQSSASEETVLRSDAPDSTGDQPGLHQENSSNGKSE-WSDASQKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSGK------GGEARLGQQGSVPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *SSSKPAGADSTHKVPVV--MLEPIRIKQ--ENSGPPENYDFPVVIVKQESDEESRPQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SASVQRAVAMSSGDVPGARGAVEGILIQQVFESGGSKK-----CIQVGGEFYTPSKFEDS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPPSNRTVQ-----SPNSSVPSPGLAGPVTMTSVHPPIRSPSASSVGSRGSSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLPTKRKASEEARAAAPAALTPR-GTASPGSQLKAKPP-KKPESSAEQQRLPLGNGIQTM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSPMIDLSAPVGGSYN-----LPSLP-DIDCSSTIMLDNIARKDTGVDHA---QP 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosomal translocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 217; DB 1;
Pred. No. 5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BREAKPOINT FOR TRANSLOCATION TIF1A-BRAF ONCOGENE.
MISSING (IN SHORT ISOFORM).
MW; 610584C1C6885972 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHD-TYPE.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
BROWDDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLN.
POLY-SER.
NUCLEAR RECEPTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOX-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein;
                                                            homolog (CHD-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SITE (NRBS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00298; CHROMO; 2.

SMART; SM00487; DEXDC; 1.

SMART; SM00490; HELICC; 1.

SMART; SM00490; HELIC; 2.

SMART; SM00249; PHD; 2.

SMART; SM00184; RING; 2.

PROSITE; PS00598; CHROMO_1; FALSE_NEG.

PROSITE; PS50013; CHROMO_2; 1.

PROSITE; PS500690; DEAH_ATP_HELICASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF308444; AAG29837.1; -.
EMBL; 267884; CAA91810.1; -.
EMBL; 267881; CAA91810.1; JOINED EMBL; 267881; CAA91798.1; -.
EMBL; 267884; CAA91798.1; JOINED WormPep; T14G8.1; CE03657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00385; Pfam; PF00628; 
                                                                                                                        DOMAIN
NP_BIND
SITE
                                                                                                                                                                                                                                       ZN_FING
                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                        ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01359;
                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                     Chromatin
                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF0027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000953; Chromo.
InterPro; IPR001410; DEAD.
InterPro; IPR002464; DEAH_box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restricuse by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
-!- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
-!- SIMILARITY: CONTAINS 2 CHROMO DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The C. elegans Mi-2 chromatin-r cell fate determination."; Development 127:5277-5284(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHD-3 OR T14G8.1.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matthews P., McMurray A.; Submitted (NOV-1995) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mueller F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20530482;
                                                                                                  Julator; Nu.

gulator; Nu.

; Zinc-finger

59
62
265
312
328
375
328
375
373
476
373
476
501
583
1287
1287
1287
763
AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitted (NOV-1995) to the EMBL/GenBank/DDBJ databases FUNCTION: Chromatin-remodelling protein that functioned fate determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zelewsky T., Palladino
                                                                                                                                                                                                                                                                                                                                                      PS50016; ZF_PHD_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elegans Mi-2 chromatin-remodelling
                                                                                                                                                                                                                                                                                                                                 regulator; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001650; Helicase_C.
IPR000330; SNF2_N.
IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    helicase_C;
chromo; 1.
PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNF2_N; 1.
                                                                                                                                                                                                                                                                                                                                                                              ZF_PHD_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11076750;
                                                                                                  205254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                  7.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED
                                                                                                               POLY-LYS.
PHD-TYPE 1.
PHD-TYPE 2.
CHROMO 1.
CHROMO 2.
POLY-ARG.
ATP (POTENTIAL).
DEAH BOX.
                                                                                                                                                                                                                                                                                                                                                    . .
                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F., Brunschwig
                                                Score 206;
                                                                                                                                                                                                                                                                                                                         protein; Repeat; Helicase; DNA-binding;
                                                                                           1EFCE1FFECE59740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no restrictions ong as its content is in
                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K., Tobler H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins function in
                                             Length 1787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              function
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Query Match Best Local S Matches 85

Similarity

7.5%; 27.2%; 116656

Conservative

46;

606

VARSPLIC SEQUENCE

510

WW.

DOMAIN SITE

DOMAIN

DOMAIN ZN\_FING

DOMAIN

DOMAIN ZN\_FING ZN\_FING ZN\_FING

RESULT 9
CHD3\_CAEEL
ID CHD3\_C
AC Q22516
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUN
DE Chromo

В Ş

814

283 755 240 700 185 652 127

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В õ

LSKPEVDYDCDVP ATVQEVQPRAEEP 355

886

Best Local

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RESULT 10
LY10_HUMAN
ID LY10_H
AC Q13342
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUN
DE LYSP10
OC LYSP10
OC Eukary
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
RA MEDLIN
RA MEDLIN
RA Dent AS
RT Class
RT Glas
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Bloch D.B., de la Monte S.M., Guigaouri P., Filippov A., Bloch K.D.; "Identification and characterization of a leukocyte-specific component of the nuclear body.";
J. Biol. Chem. 271:29198-29204(1996).
-I- FUNCTION: COMPONENT OF THE NUCLEAR BODY, ALSO KNOWN AS NUCLEAR DOMAIN 10, PML ONCOGENIC DOMAIN, AND KR BODY. MAY BE INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q13342; Q13341; Q92881;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
12-JUN-2002 (Rel. 41, Last annotation update)
13-JUN-2002 (Rel. 38, Created)
13-JUN-2002 
                                                                                                                                                                                     TISSUE=Placenta;
MEDLINE=97067175; PubMed=8910577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS LYSP100-A AND LYSP100-B) MEDLINE=96329578; PubMed=8695863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM SP140).
                                                                                                                                                                                                                                                                                                                              Blood 88:1423-1426(1996).
                                                                                                                                                                                                                                                                                                                                                                       bodies
                                                                                                                                                                                                                                                                                                                                                                                           class of
                                                                                                                                                                                                                                                                                                                                                                                           "LYSP100-associated nuclear domains (LANDs): class of subnuclear structures and their rela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dent A.L., Yewdell J., Puvion-Dutilleul F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYSP100 OR SP140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 KILSWRWKEISYPEPLECKEGEEASKDDVFLKPP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 VTKMYPLFQVKYKEF------QDHMTAHGKSI-----QKQQRAKFVP---VPVPVTPQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCDGCPRAFHLACLSPPLREIPSGTWRCSSCLQATVQEVQPRAEEPRPQEPPVETPLPPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APGARCGVCGDGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSGDVTPAP---VE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGPKPLVRAKGAQGAAPGGGEARLGQQGSVPAPLALPSDPQLHQKNEDECAVCRDGGELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSPARLAPG - - PAKDDTASHEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koken M.H.M.,
                                                                                                                                                                                                                                                                                                                                                                                       description ationship to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         de The H.,
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                                                                                                                                                                                                                                                                                                                                                                                           nuclear
                                                                                                                               component
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                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00297; BROMO;
SMART; SM00249; PHD; 1.
SMART; SM00258; SAND; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
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Pfam; PF00439;
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ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E; PS00633; BROMODOMAIN_1; F

E; PS50014; BROMODOMAIN_2; 1

E; PS50864; SAND; 1.

E; PS01359; ZF_PHD_1; 1.

E; PS50016; ZF_PHD_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGNC:17133; SP140
                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR004865;
IPR001965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001487;
IPR000770;
                                                                                                                                                             882
                                 Conservative
                                                                                                                                                                                                                          447
219
838
862
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; Sp100; 1.
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221
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882
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829
297
400
386
446
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661
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SUBCELLULAR LOCATION: LOCALIZED TO NUCLEAR STRUCTURES TERMED
                                                                                                       THE PATHOGENESIS
                                                                                                     OF ACUTE PROMYELOCYTIC LEUKEMIA AND VIRAL
                     GLOBULAR,
BUT
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LANDS, FOR LYSP100-ASSOCIATED NUCLEAR DOMAINS. LANDS ARE GLOBUI ELECTRON-DENSE STRUCTURES MOST OFTEN FOUND IN THE NUCLEOPLASM, ALSO FOUND AT THE NUCLEAR MEMBRANE AND IN THE CYTOPLASM, SUGGESTING THAT THESE STRUCTURES MAY TRAFFIC BETWEEN THE CYTOPLASM

HERE) AND SP140; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGH LEVELS IN SPLEEN AND PERIPHERAL BLOOD
LEUKOCYTES, MUCH LOWER LEVELS IN THYMUS, PROSTATE, OVARY, SMALL
INTESTINE, AND COLON. VERY LOW LEVELS IN HEART, BRAIN, PLACENTA, 3 ISOFORMS; LYSP100-A, (SHOWN

LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, AND PANCREAS

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-!- INDUCTION: BY INTERFERONS.
-!- DISEASE: THIS ANTICEN IS RECOGNIZED BY AUTOANTIBODIES FROM PATIENTS WITH PRIMARY BILIARY CIRRHOSIS.
-!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
-!- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 1 SAND DOMAIN.

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bromodomain; Bromodomain. SAND\_domain. Znf\_PHD Sp100

Bromodomain; DNA-binding; Alternative splicing;

FALSE\_NEG

MW. MISSING MISSING MISSING (IN ISOFORM LYSP100-A).
MISSING (IN REF. 2).
G -> D (IN REF. 2). SSSLARRGSVSSELENHPMNEEGESEELASSLLYDNVPGAE Q -> QKQGRKVIKRVAQWILWILQTTPLWENPRGKEEKRG GMAGAE (IN ISOFORM LYSP100-A). GNKWEQLTGLVDAESIQQMAP -> ETNGNN (IN MISSING PHD-TYPE. NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). SAND. BROMODOMAIN POLY-TYR A3251FEBB7005560 (IN ISOFORM SP140). (IN ISOFORM SP140). (IN ISOFORM LYSP100-A) CRC64; REF

7.0**%**; 33.5**%**; 21; Score 204.5; Pred. No. 0.0 Mismatches 1.0002; 63; DB 1; Indels Length 882; 39; Gaps

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TESTULATION ACCORDED TO THE CONTROL OF THE CONTROL 
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-I- FUNCTION: SEEMS TO ACT AS A TRANSCRIPTIONAL REF-
I- SUBCELLULAR LOCATION: Nuclear (By similarity).
-I- ALTERNATIVE PRODUCTS: 2 isoforms; Alpha (shown are produced by alternative splicing.
-I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-I- SIMILARITY: CONTAINS 2 B BOX-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                    Kikuno R., Nagase T., Ishikawa K. I., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which for large proteins in vitro."; DAA Res. 6:197-205(1999).
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                                                                                                                                                                     Oncogene 18:4388-4393(1999)
                                                                                                                                                                                                   to the ret receptor tyrosine carcinomas.";
                                                                                                                                                                                                                                                                                                    MEDLINE=99367902; PubMed=10439047;
                                                                                                                                                                                                                                                                                                                                       TISSUE=Thyroi
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 76-1127 FROM N.A. (ISOFORM ALPHA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UPN9; Q9C855; Q9UJ79; Q9C017;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription intermediary factor 1-gamma (TIF1-gamma) (RET-fused
7 protein) (Rf67 protein) (Tripartite motif protein 33).
                                                                                                                                                                                                                                                                                Klugbauer S., Rabes H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Luzi Riganelli D., Zanaria E., Messali S., Cainarca S., Guffanti Minucci S., Pelicci P.G., Ballabio A.; "The tripartite motif family identifies cell compartments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDLINE-99144725; PubMed-10022127;
Venturini L., You J., Stadler M., Galien R., La
Koken M.H.M., Mattei M.-G., Ganser A., Chambon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99397452; PubMed-10470851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
MEDLINE-21231161; Pubmed-11331580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene 18:1209-1217(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "TIF1gamma, a novel member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The H.;
                                                                                                                                                                                                              transcription coactivator htifl and a related protein he ret receptor tyrosine kinase in childhood papillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. 20:2140-2151(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCPEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPVTCGGVKGILHKKKLQQGILVKCIQTEDGKWFTPTEFEIKG----GHARSKNW-RLSVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                    TO ACT AS A TRANSCRIPTIONAL REPRESSOR.
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M.-G., Ganser A., Chambon P., Losson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the transcriptional intermediary factor
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Guffanti A.,
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                                                                                  Beta;
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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PRO1406; BBOXZNFING
PRINTS; PRO0503; BROMODOMAI
SMART; SM00502; BBC; 1
SMART; SM003036; BBOX; 2
SMART; SM00336; BBOX; 2
SMART; SM00299; BROMO; 1
SMART; SM00299; BROMO; 1
SMART; SM00249; BRO; 2
SMART; SM00184; RING; 2.
                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                        VARSPLIC CONFLICT
                                                                                                                                                                                                             ZN_FING
DOMAIN
                                                                                                                                                                                                                                                       ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00633; BROMODOMAIN_1; FALSE_NEG.
PROSITE: PS50014; BROMODOMAIN_2; 1.
PROSITE: PS50119; ZF_BBOX; 2.
PROSITE: PS01359; ZF_PHD_1; 1.
PROSITE: PS50016; ZF_PHD_2; 1.
PROSITE: PS50018; ZF_RING_1; 1.
PROSITE: PS50089; ZF_RING_2; 1.
                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
752 GSCGSSGRT---AEKTSLSFKSDQVKVKQEPGTEDEICSFSGGVKQEKTEDGRRSACMLS
                     175 LPLGNGIQTMSASYQRAVAMSSGDV----PGARGAV---EGILIQQVFESGGSKKCIQV
                                                 710
                                                                     115
                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                            Alternative
                                                                                                                                                                                                                                                                                                                       Zinc-finger;
                                                                                                                                                                                                                                                                                                                             Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 605769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T04946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003649;
                                                              PPAVPKALVPPPRLPTKRKASEEARAAAPAALTPRGTASPGSQLKAKPPKKPESSAEQQR
                                                 PPQPTSTMNPSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 BROMODOMAIN. SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pro; IPR001841; Znf_ring.
PF00097; zf-C3HC4; 1.
PF00439; bromodomain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB029036; BAA83065.1; ALT_INIT.
AJ132948; CAB55313.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF119043; AAD17259.1;
AF220136; AAG53509.1;
AF220137; AAG53510.1;
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:16290; TRIM33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001487;
IPR000315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001965;
                                                                                                                                             1041
89
451
909
1037
                                                                                                                                                                                                                                             125
212
271
299
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                          splicing
                                                                                                                                                                                                                                                                                                                  Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zf-B_box; 2.
                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHD;
                                                                                                                                             18
49
154
259
312
401
550
934
1046
1089
939
1037
1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BROMODOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BBOXZNFINGER.
                                                                                                                                  122521
                                                                                                   25.98;
                                                                                                            7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bbox_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Znf_Bbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bromodomain.
                                           -----GPSALSP---GSSGLSNSHTPVRPPSTSSTGSR
                                                                                                                                                                                                                                                                                                                            Repressor; DNA-binding; Bromodomain;
                                                                                        34;
                                                                                                                                  MW;
                                                                                      Score 204; DB
Pred. No. 0.000
34; Mismatches
                                                                                                                                                      PAA -> LLH
F -> S (IN )
R -> T (IN )
                                                                                                                                                                                                                                                    POLY-GLU.
RING-TYPE.
B BOX-TYPE
B BOX-TYPE
                                                                                                                                        F -> S (IN REF. 4).

R -> T (IN REF. 1).

RKRLKSDERPVHIK -> QKTPKVR (IN
                                                                                                                                                                                    BROMODOMAIN.
MISSING (IN ISOFORM BETA).
V -> E (IN REF. 4).
                                                                                                                                                                                                                        PHD-TYPE.
                                                                                                                                                                                                                             POLY-THR.
                                                                                                                                                                                                                                        COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                               POLY-GLY
                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                02E3880CFDCFDA3B CRC64;
                                                                                                                                                                                                                                                                                                                   Coiled coil;
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.00027;
                                                                                                                                                                         (IN REF. 4).
                                                                                       101;
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                                                                                     60;
                                                                                                                                           REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a collaboration
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                                                                                                                                                                                                                                                                                                                                                                        RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinovitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Vonstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goifeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RT "The genome Sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _SCHPO
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Q09698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., Oneil S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., Oneil S., Mungall K., Murphy L., Niblett D., Odell C.,
                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
InterPro; IPR001965; Pfam; PF00628; PHD; SMART; SM00249; PHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPAC2F7.07C
                                                                        EMBL; Z50142; CAA90494.1;
                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: TO S.POMBE SPAC16C9.05 AND YEAST YMR075W-!- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002
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                                                                                                                              email to license@isb-sib.ch).
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updat
1 protein C2F7.07c in chromosome
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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., As Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Ra Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Ra Brooks K., Brown D., Brown S., Chillingworth T., Fraser A., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Ra Holroyd S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Jones K., Jones M., Leather S., McDonald S., McLean J., Sander S., Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., A., A., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., A., A., Mooney P., Moule S., Bearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Sanders D., Seeger K., Sharp S., Sandors D., Walsh S.V., Warren T., Whitehead S., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Ra, Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
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ZN_FING 263 31
ZN_FING 406 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat)
Hypothetical protein C16C9.05 in chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01359; ZF_PHD_1; PROSITE; PS50016; ZF_PHD_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPAC16C9.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YAC5_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 TASPGSQLKAKPPKKPESSAEQQRLPLGNGIQTMSASVQRAVAMSSGDVPGARGAVEGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   476 SGDVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQQVFESGGSKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDHVTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SISSFFRGVGSGVMGEYIE-----TDVLKHLKSSRRSNGEERDPLL-LKSKSGTPILC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLPDDAWYCNECKHHSLYNELDEQEELESNVKEEGTMVDVWMQLCTYIDSHNPIQFHLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRNVTVYSNQK---HLGNE---SENFNDM---EGRAEDISSNELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGPEGQQNLAPGARCGVCG-DGTDVLRCTHCAAAFHWRCHFPAGTSRPGTGLR---CRSC
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406
607 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 32, Created)
(Rel. 32, Last seq
(Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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459
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Best Local
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 SEQUENCE FROM N.A.
MEDLINE=84270667; PubMed=6087149;
Baer R., Bankier A.T., Biggin M.D.,
Gibson T.J., Hatfull G., Hudson G.S.
                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical BHLF1 protein.
Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                Gammaherpesvirinae; Lymphocryptovirus
                                                                                                                                                                                                 P03181;
21-JUL-1986
                                                                                                                                                                                                                                                       EBV.
                                                                                      NCBI_TaxID=10377;
                                                                                                                                                                                                                                    YHL1_EBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Gofffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Lucas M., Rochet M., Gaillardin C., Hunt C., Moore K., Hurst S.M.,
Luga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Deminguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
Wature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                          307 LNPKVMISGWQFLMGEFPSDELL 329
                                                                                                                                                                                                                                                                                                                                          508 -EPALHRDDLESLLSEHTFDGIL 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 254366; CAA91193.1;
InterPro; IPR001965; Znf_I
Pfam; PF00628; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; ZN_FING 117 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01359; ZF_PHD_1; 1. PROSITE; PS50016; ZF_PHD_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 -----PKHPLSIWSQLYDWIDSQNPSQYRLPDDLVHYFHGISRGDTGAYKETEGEMDT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00249; PHD;
                                                                                                                                                                                                                                                                                                                                                                                                                             352 AEEPRPQEP------PVETPLPPGLRSAGEEV-RGPPG---EPLAGMDTTL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 RNVDYCSACGGRGLFICCEGCPCSFHLSCLEPPLTPENIPEGSWFCVTC---SIKSHHP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 KNEDECAVCRDGGELICCDGCPRAFHLACLSPPL--REIPSGTWRCSSCLQATVQEVQPR 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQONLAPGARCGVCGDGTD----VLRCTH 448
                                                                                                                                                                                                                                                                                                                                                                               CDTFYHKNCKEHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
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                                                                                                                                                                                                                               STANDARD;
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     Hudson G.S.,
                                                                                                                                                                                                                                                                                                                                                                   ---KKCSHD--SIGKKGMRVPKNAVVIRTPLVLDTTSNT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 179.5; DB Pred. No. 0.0022;
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Deininger P.L., Farrell P.J., ., Satchwell S.C., Seguin C.,
                                                                                                                                                                                                                             660 AA
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          YMW5_YEAST STANDARD; PRT; 684 AA.
Q04779;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 78.8 kDa protein in ABF2-CHL12 intergenic region.
YMR075W OR YM9916.14.
                                                                                                                              _YEAST
                                                                                                                                                                                          584
                                                                                                                                                                                                                492 PARLAP----GPAKDDTAS-----HEPALHRD 514
                                                                                                                                                                                                                                           524 SARNPGCPRTWRRRSGAQRGHPPPGAGQRPSGPTGGRPAAPGAPGTPAAPGPGGGAAVPS 583
                                                                                                                                                                                                                                                                          443 VLRCTHCAAAFHWRCHFPAGTSRPGTGLRCRSCSG------DVTPAPVEGVLAPS 491
                                                                                                                                                                                                                                                                                                        464 PERGSGPADPPAAARLPPERQEPRLPQDLAAAQRCPAGPPPTRSGAAAQRTHRRPPGCPR 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     416
                                                                                                                                                                                                                                                                                                                                                                                                                                    376 G-----PPPTRSGAAAQRTHRRPPGCPRSARNPGCPRTWRRRSGAQ-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 AFHLACLSPPLR------EIPSG------TWRCSSCLQATVQEVQPRAEEP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 AQG--AAPGGGEARLGQQGSVPAPL--ALPSDPQLHQKNEDECAVCRDGGELICCDGCPR 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 RRSGAQRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 ---GAVEGILIQQVFESGGSKKCIQVGGEFYTPSKFEDSGSGKNKARSSSGPKPLVRAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 AARLPPERQEPRLPQDLAAAQRCPAGPPPTRSGAAAQRTHRRPPGCPRSARNPGCPRTWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 QLKAKP----PKKPESSAEQQRLPLGNGIQTMSASVQRAVAMSSGDVPGAR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 PGAGQRPSGPTGGRPAAPGA----PGTPA--APGPGGGAAVPSGATPHPERGSGPADPPA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 PRKGRKP-----PAVPKALVPPPRLPTKRKASEEARAAAPAALTPR-----GTASPGS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A03742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; V01555; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                GATPHPERGSGPADPPAAARLPPERQEPRLPQD 616
                                                                                                                                                                                                                                                                                                                                        PLLCVG-----PEGQ-----QNLAPGARC-----GVCGDGTD-----
                                                                                                                                                                                                                                                                                                                                                                        RGHPPPGAGQRPSGPTGGRPAAPGAPGTPAA-----PGPGGGAAVP--SGATPH
                                                                                                                                                                                                                                                                                                                                                                                                      RPQEPPVETPLPPGLRSAGEEVRGPPGEPLAGMDTTLVYKHLPAPPSAAPLPGLDSSALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APGTPAAPGPGGGAAVPSGATPHPERGSGPADPPAAARLPPERQEPRLPQDLAAAQRCPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      660 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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23.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Early protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 168.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---HPP----PGAGQ-RPSGPTGGRP--AAPG
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AA TANDEM REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192;
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Saccharomyces

cerevisiae (Baker's yeast)

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
SGD; S
                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01359; ZF_PHD_1; 1.

PROSITE; PS0016; ZF_PHD_2; 1.

Hypothetical protein; Zinc-finger.

Hypothetical 260 309 PHD-T

DOMAIN 15 30 POLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pearson D., Bowman S., Barrell B.G., Rajandream M.A., Walsh Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
-i- SIMILARITY: TO S.POMBE SPACIGG9.05 AND SPAC2F7.07C.
-i- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID-4932;
[1]
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD; S0004680; YMR075W.
InterPro; IPR001965; Zn
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
426
                                    440
                                                                       378 KIPLTDRQLFNTSYGQSITKLDSYNPDTHIDSNSGKFLICY----
                                                                                                             384
                                                                                                                                                318
                                                                                                                                                                                    344
                                                                                                                                                                                                                     258 ENEDFCSACNOSGSFLCCDTCPKSFHFLCLDPPIDPNNLPKGDWHCNECKFKIFINNSMA 317
                                                                                                                                                                                                                                                         294 KNEDECAVCRDGGELICCDGCPRAFHLACLSPPL--REIPSGTWRCSSC------LQA 343
GSWSHPENSRLIMTCDYCQTPWHLDCVPRASFKNLGSKWKC
                                GT------DVLRCTHCAAAFHWRCHFPAGTSRPGTGLRC 472
                                                                                                         --PLAG--MDTTLVYKHLPAPPSAAPLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGD 439
                                                                                                                                            TLKKIESNFIKQNNNVKIFAKLLFNIDSHNPKQFQLPNYIKETFPAVKTGSRGQYSDEND
                                                                                                                                                                                TVQEVQPRAEEPR------PQEPPVETPLPPGLRSAGEEVR-GPPGE-----
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                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                          h 5.5%; Score 161; DB 1; Length 684; Similarity 21.7%; Pred. No. 0.038; 48; Conservative 34; Mismatches 85; Indels !
                                                                                                                                                                                                                                                                                                                                                                   684 AA; 78836 MW; CFC282DC9A782E5C CRC64;
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466
                                                                     -- KCNQTRL 425
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